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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

REFERENCE AUTHORS TITLE JOURNAL FEATURES SOURCE CDS	RESULT 1 A96985 LOCUS DEFINITION ACCESSION VERSION KEYWORDS		C 45	43	40 41	39	37 38	C 35		C 31	c 29 30	28		24 1 25 1		20 1 21 1			٠.						, U	ພ 4 . ພ ພ	2 1	Result No. S
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Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
1 (bases 1 to 1179)
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Lescure,B., Van Montayu,M., Engler,G. and Inze,D.
A new D-type cyclin of Arabidopsis thaliana expres
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/product="D-type cyclin"
/protein_id="Cab41347.1"
/protein_id="Cab41347.1"
/db_xref="G1:4688615"
/dtanslation="MaedileLicTesnvddegmivDerpieisipomgesosese
Elimenvekschlepsdyirklrsgdldlnvgrrdalnwiwkacevhofeplcfcla
MNYLDRFLSVHDLPSGKGWILQLLAVACLSLAAKIEETEVPMLIDLQVGDPQFVFEAK
SYQRMELLVLNKLKWRLBAITPCSYIRYFLKMSCDGEPSNTLISRSLQVIASTTKG
IDFLERRPSEAAAVALSVSGELQFVHEDNSSESPLFSLLQKERVKKIGEMIESDGSD
LCSQTPNGVLEVSACCFSFKTHDSSSSSYTHLS"

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/db_xref="taxon:3702"
118. 1044
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118. .1044
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/codon_start=1
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Pred. No. 5.6e-222;
Mismatches 0;
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Sequence 1 :
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A85057.1 G:
                        MUTTAY, J.A.
PLANTS WITH MODIFIED GROWTH
PATENT: WO 9842851-A 1 01-OCT-1998;
MURRAY JAMES AUGUSTUS HENRY (GB); U
                                                                     common tobacco.
Nicotiana tabacum
Nicotiana tabacum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids I; Solanales; Solanaceae; Nicotiana.
                                                               (bases 1 to 1284)
                Location/Qualifiers
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AJ011892 GI:-
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Nicotiana tabacum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids I; Solanales; Solanaceae; Nicotiana.

1 (bases 1 to 1284)
Murray, J.A. H.
Direct Submission
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TGCTCATACATAAGATATTTCCTGAGAAAGATGAGTAAATGTGATCAAGAACCATCCAAC
                                   CAAAGAATGGAACTTTTGGTATTAAGCACATTGAAGTGGAGAATGCAAGCTTATACACCT 781
                                                        CAAAGAATGGAGCTTTTGGTGTTGAACAAATTGAAATGGAGATTGAGAGCAATAACTCCA
                                                                                                       CCTTTGACTGTTGATTTACAGGTAGGGGATCCCAAATTTGTATTTGAAGGCAAAACTATA 721
                                                                                                                          CCAATGTTGATAGATCTTCAGGTTGGAGATCCTCAGTTTTGTGTTTTGAGGCTAAATCAGTC 486
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                                                                                                                                                                                                                                                                                                              GATTGGATTTTGAAGGCTCATATGCACTATGGATTTTGGAGAGCTGAGTTTTTGTTGTCG
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Distinct cyclin D genes show mitotic accumulation or collevels of transcripts in tobacco bright yellow-2 cells plant Physiol. 119 (1), 343-352 (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               University of Cambridge, Tennis Court Road, Co
2 (bases 1 to 1284)
Sorrell,D.A., Combettes,B., Chaubet-Gigot,N.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (07-OCT-1998) Murray J.A.H., Institute of Biotechnology, University of Cambridge, Tennis Court Road, Cambridge, CB2 1QT, UK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /translation="MAADNIYDFVASNILCTETKSLCFDDVDSLTISQQNIETKSKDL

SFNNGIRSEPLIDLPSLSEECLSFMYQREMEFLPKDDYVERLRSGDLDLSVRKEALDW

ILKAHMHYGFGELSFCLSIVLDRFLSLYLELPRSKTWTVQLLAVACLSLAAKMEEINV

PLTVDLQVGDFFEKTIQRMELLYLSTLKMRMQAYTPYTFIDYFMKKMNGDQIPS

RPLISGSMQLILSIIRSIDFLEFRSSEIAASVAMSVSGEIQAKDIDKAMPCFFIHLDK

GRVQKCVELIQDLTTATITTAAAASLVPQSPIGVLEAAACLSYKSGDERTVGSCTTSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="LxCxE motif"
464. .781
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="Cyclin Box"
179 c 261 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /gene="CycD2.1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /product="cyclin D2.1 protein"
/protein_id="CAA09852.1"
/db_xref="GI:4160298"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        gene="CycD2.1"
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182. .1246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Nicotiana tabacum"
/db_xref="taxon:4097"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /cell_line="Bright Yellow 2 (BY-2)"
/dev_stage="exponentially growing cells"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AGAGTACACTTTGACAACTCTTCCTCTCTCTCTCTTTTCTCACAACTTCTAAAAGGAGAGA 786
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4 (bases 1 to 1650)
Murray, J.A.H.
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                                                                                                                                                                                                                                      Direct Submission

Direct Submission

Submitted (19-MAR-1998) J.A.H. Murray, Inst. of Biotechn.,Univ. Cambridge, Tennis Court Road, Cambridge, CB2 1QT, UK

On Mar 28, 1998 this sequence version replaced gi:1402895.

Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                  Murray, ......
Direct Submission
Submitted (07-JUN-1996)
Submitted (07-JUN-1996)
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Submitted (08 DEC-1994) J.A.H. Murray, Inst.
Cambridge, Tennis Court Road, Cambridge, CB2
Revised by [3]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      by growth regulators and containing the conserved retinoblastoma protein interaction motif Plant Cell. 7 (1), 85-103 (1995)
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A.thaliana mRNA for
X83370
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1 (bases 1 to 1650)
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CycD2; cyclin; cyclin
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/codon_start=1
/product="cyclin delta-2"
/protein_id="CaA58286.1"
/protein_id="CaA58286.1"
/db_xref="G1:295132"
/db_xref="SWISS-PROT:P42752"
/translation="MAENLACGETSESWIIDNDDDDINYGGGFTNEIDYNHQLFAKDDNFGGNGSIPMMGSSSSSLSEDRIKEMLVREIEFCPGTDYVKRLLSGDLDLSVRNQALD
                                                                                                                                         /dev_stage="seedlings,
/tissue_type="whole see
/clone_lib="pFL61"
                                                                                                                                                                                      /variety="ecotype Landsberg
/db_xref="taxon:3702"
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Road, Cambridge, CB2
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811 GAGAGT
                                                                                                                                                                                                                                                                                                                                                                   762
                                                                                                                                                                                                                                                                                                                                                                                                                                                   702
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  94 TCGATTCCTCAGATGGGTTTTTCTCAATCG----GAGAGTGAGGAGATTATCATGGAGATG 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local
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                                                                                                                                                                                                                                                                                                                                                                                        GAAGATCCCAAGTTTGTTTTTGAGGCCAAAACAATAAAAAGGATGGAGCTTTTGGTTGTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GGAGATCCTCAGTTTGTGTTTTGAGGCTAAATCAGTCCAAAGAATGGAGCTTTTTGGTGTTTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CATTACCATTTTGGACATCTGTGCATATGCCTATCCATGAACTACTTGGATCGGTTCTTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GTACACCAGTTTGGACCATTGTGTTTTTGCTTAGCAATGAACTACTTGGATCGATTCTTA 330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GATTTGGATTTGAATGTTGGAAGAAGAAGATGCCCTCAATTGGAATTTGGAAGGCTTGTGAA 270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TTGGTGAGAGAGTTTGAGTTTTGCCCCTGGAACTGATTATGTTAAGAGATTGCTTTCTGGT 464
                                        GCACTGTCTAGTCTCATATATGTAAAACAGGAGAGGGTGAAGAAGATGTTTGAATCTGATG
                                                                                                                                                            GCTGCTGTGGCACTTTCTGTTTCTGGAGAATTGCAGAGTACACTTTGACAACTCTTCC
                                                                                                                                                                                                  TTCATCTTAAACACCACCAAAGCAATTGAATTCTTAGACTTCAGGCCTTCTGAGATAGCT
                                                                                                                                                                                                                                          GTGATAGCCAGCAACCAAAGGTATTGACTTTTTGGAGTTTAGACCTTCTGAAGCTGCT 690
                                                                                                                                                                                                                                                                                     GACAAGATCAG-----TGGTCACGTGTCGGAGAATTTGATCTATAGATCGTCAAGA
                                                                                                                                                                                                                                                                                                                         AGAAAGATGAGTAAATGTGATCAAGAACCATCCAACACATTGATATCTAGATCATTACAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TTATCATTGGCAGCCAAAATTGAAGAAACTGAAGTTCCAATGTTGATAGATCTTCAGGTT 450
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ACATCCTATGAATTGCCGAAAGACAAGGATTGGGCTGCTCAGTTACTAGCTGTGTCTTGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TCGGTTCATGATTTGCCTAGTGGCAAAGGTTGGATATTGCAGTTGTTGGCTGTGGCTTGT 390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TCAATTCCGATGATGGGTTCTTCATCGTCCTTGAGTGAAGACAGAATCAAAGAGATG
                                                                              TTCTCTCCTCTTTTCTCACTACTTCAAAAGGAGAGAGTGAAGAAGATAGGGGAAATGATA 810
                                                                                                                      GCAGCTGCTGCAGTGTCTGTTTCCATTTCAGGAGAAACAGAATGCATTGATGAGGAAAAG
                                                                                                                                                                                                                                                                                                                                                                   ACCACTTTGAATTGGAGATTGCAAGCTCTAACTCCATTCTCCTTCATTGATTATTTCGTT
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/note="pest motif, potential"
a 293 c 346 g 483 t
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ESCTNSSQSSPDNNNNNNNSNKRRRKQ"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VPHIVDLQVEDPKFVFEAKTIKRMELLVVTTLNWRLQALTPFSFIDYFVDKISGHVSE
NLIYRSSRFILNTTKAIEFLDFRPSEIAAAAAVSVSISGETECIDEEKALSSLIYVKQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WILKVCAHYHFGHLCICLSMNYLDRFLTSYELPKDKDWAAQLLAVSCLSLASKMEETD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="pest motif, 480. .798
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="cyclin box"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note=
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "pest
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Pred. No. 2.8e-56;
0; Mismatches 250;
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AB011479/c
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MEDLINE
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                                                                                                                                                                                                                                                                                                                               CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    protein similarity are described as 'unknown protein'.

The software programs used to predict genes include: Grail
(Informatics Group, Oak Ridge National Laboratory,
http://compbio.ornl.gov/crail-1.3/),
GENSCAN (Chris Burge, MIT, http://CCR-081.mit.edu/GENSCAN.html),
NetGene2 (S.M. Hebsgaard, et al., CBS, Technical University of
Denmark, http://www.cbs.dtu.dk/services/NetGene2/) and
Splicepredictor (Volker Brendel, Stanford University,
http://gremlinl.zool.iastate.edu/cgi-bin/sp.cgi).
Genes encoding tRNAs are predicted by tRNAscan-SE/).
Genes didy, Washington University School of Medicine, St. Louis,
http://genome.wustl.edu/eddy/tRNAscan-SE/).
This sequence may not be the entire insert of this clone. It may be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Direct Submission
Submitted (02-MAR-1998) Yasukazu Nakamura, Kazusa DNA Research
Institute, Department of Plant Gene Research; 1532-3, Yana,
Kisarazu, Chiba 292-0812, Japan (E-mail:ynakamu@kazusa.or.jp,
Tel:81-438-52-3935, Fax:81-438-52-3934)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Arabidopsis thaliana go
AB011479 BA000015
AB011479.1 GI:2924729
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       http://www.kazusa.or.jp/kaos/cgi-bin/agd_graph.cgi?c=MNA5
Genes with similarity to proteins in the databases are described in 'product' or 'note' qualifiers. Genes that have no significant protein similarity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence features of the regions of 1,381,565 one physically assigned P1 and TAC clones DNA Res. 5 (2), 131-145 (1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Arabidopsis thaliana (strain:Columbia) DNA, clone_lib:Mitsui clone:MNA5.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Kaneko, T.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 for correspondence: kaos@kazusa.or.jp
                                                                                                                                                                                                                                          /clone_lib="Mitsui P1"

join(1713. .1880,2399. .2487,2807. .2965,3195. .3408,

3700. .3786,3869. .4008,4139. .4219,4336. .4400,4559.

4865. .4995,5074. .5155,5262. .5475,5585. .5665,5742.

/note="gene_id:mNA5.1"
                                                  /translation="MMVFYLISLPLTLGLVVFTLRYFAGPEIPRYVLITVGYTWFCSVSVIILAPADIWTTLSLQPDHPENGAISFLWSWSYWSTFLLTWAVVPLIQGFEDAGDFT
                                                                                                        /evidence=not_experimental
/protein_id="BAB11551.1"
/db_xref="GI:9759609"
                                                                                                                                                                                                                      unknown
FLLGFGLSEIPKTLWKNADWTTRQKVLSHKIAKIAVKLDNAHQELSNAIVVAQATSTQ
                            VSERLKTSVHVNLVFYLVLGFIGLLGLILLIMMHRNWTGSILGYAMACSNTFGLVTGA
                                                                                                                                                                                                                                                                                                                                                                               /clone="MNA5"
                                                                                                                                                                                                                                                                                                                                                                                                           /chromosome="5"
                                                                                                                                                                                                                                                                                                                                                                                                                                        /db_xref="taxon:3702"
                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Arabidopsis
/strain="Columbia"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
                                                                                                                                                                                          /codon_start=1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          . 88356
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       фþ
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/note="gene_id:MNA5.6
pir||T13016
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /translation="mmfQQDYPHGFSLVETSLSYEMLDYFQNIVVSNSEDVASQONSI
SSSSYSASTLSCSITECKSHLTEKLSPLRERYGCGDFLSRKRRRSEKTIVDKENQRM
NHIAVERNRRKGMNHFLSILKSMMPLSYSQPNDASILEGTISYLKKLEORLQSLEAQ
LKATKLNQSPNIFSDFFMFPQYSTATATATATATASSSSSSHHHHKRLEVVADVEVTMVE
RHANLKVLTKTQPRLLFKIINEFNSLGLSTLHLNLTTSKDMSLFTFSVKVEADCQLTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFVKMEEHEDLESGEEACKLFADNEOWYCSDOWNS"
complement(join(19267. .19356,19515. .19916,20141 .20:
/note="contains similarity to bHLH DNA-binding protein
gene_id:MNA5.5"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              **Translation="MKRSRGSSDSLSGFLPIRHSTTDK0ISPRPTTTGFLYSGAGDYS
OMEDALEDDGSLEDLGGVGHASSTAAEKKRRLGVEDVKALEKUREIDIKLEPERKVKL
AQELGLQPROVAIWFOGRARAWKTKQLERDGVGLKSKEDALKRNRDSLQBDUDSLLGD
KKELKAKLNVEGVKGIEENGALKAVEANQSVMANNEVLELSHRSPSPPPHIPTDAPTS
/evidence=not_experimental
/protein_id="BAB11556.1"
/db_xref="GI:9759614"
                                                                                                                                        similar to unknown protein"
                                                                                                                                                                                                                                          complement(25583.
                                                                                                                                                                                                                                                                                                                                                                        SKESLEMYNHGDATLSQLPLSAPHSNQLINYQNHLMQHGEGQNMCSDNITNNNFEHPG
                                                                                                                                                                                                                                                                                                                                                                                                   PDGELRTWPKERETYKDMALRYKEARKRKKSRNLHEFLEKEKDKDKGKTNLKKNWYPN
FDHYSPQQLSQLLQSLERTLSTLQERLRIVEAQKLQNTNLVHQSLTPSYLNQTQHLNP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           strong similarity to unknown
                                                                                                                                                                                                                                                                                                                                          VSNTQDYSPLLSVQASAVNNYGLNNHLMQQQDQLHGFDQNMCMVSEIINNNNGLQHPN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /evidence=not_experimental
/protein_id="BAB11555.1"
/db_xref="GI:9759613"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SGNEVANTVHEVVRRVHKER"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /evidence=not_experimental
/protein_id="BAB11554.1"
/db_xref="GI:9759612"
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/product="tRNA-Met(CAT)"
complement(join(14356...14)
                                                                                                                'codon_start≃1
                                                                                                                                                                                                               'note="gb|AAD22354
                                                                                                                                                                                                                                                                                                        SNTVPHEFSSDFNQNPYGNAVGNISFSQDMFSSYDASSLLQTSSLPPLHNIPSSYCF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       translation="MKQASSSSSSRNSTSLTNRLKTIFKKAEELSILCAIEVCVIYYG"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            {	t ELAFEMFSIFPRTENFRDDPADSSDSSAVLNEEYSPNTVEAAGAVAATTVEMSTMGCF}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /product="homeobox-leucine zipper protein ATHB-5
protein ATHB-5)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  sp|P46667"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="gene_id:MNA5.4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DLTKKKTEKLKSTTVKKKTGFWTKLLHLKGKGGGADVGGFVTSRQRVY"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /translation="MECRKHNHQGNRGVCPCCLRDKLSRLPNTTSYYIVHRSSSSSSTTVSSSPSSBAVKDHRRAGSMSMSFAVREALNGNLIEALGGGLMKSRSMAHVPKDYIVR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /evidence=not_experimental
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NFSENSSVEMKMSSSYDIDTIKGSSSKDDMSRKYGSAREAITNKYAAIREQQNKHSPS
SMTKPENMASAKVSILETDNSGPSNGQGSGEPSSRLASTWRNMKLGIQSFKENVATKK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                {f SWKRFRFQTETEDTDGFDPSGLMILKKERTWLEEGQKVGEHVLPLARNFNDVDIEPGS}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AKDBYRYKGBYLITYTEALYLEDITMKNYERRDATGWKYISSFRATRTGKMGNILDSL
EFMWRCILKKOIQMYLAVVMGINSAAIILAEATILLSKIDLSLESILISSYKSDELLY
QAFARVYLLYMCVCTYYSLFKIGMLMIYSLTPROTSSYNLLMICSMIARYAPPISYNL
INLIQLHSETIFEKKMGRIDDAVPVFGORFNEIYPLIMVIYTLLVASNFFDRIFNYFG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /protein_id="BAB11553.1"
/db_xref="GI:9759611"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /evidence=not_experimental
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/note="gene_id:MNA5.3"
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                                                                                                                                                                          id:MNA5.7
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121 TCGGAGAGTGAGGAGATTATCATGGAGAGGAGGAGAAGGAGAAGCAGCATTTGCCAAGT 180

GGCATGATTGTTGACGAAACTCCGATTGAAATTTCGATTCCTCAGATGGGTTTTTCTCAA 120

55530

55590

ATGGCAGAGGAAAATCTAGAACTGAGTCTTTTATGTACAGAGAGCAACGTTGATGATGAG

55589

61

55649

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Matches Query Match Best Local

263;

Conservative

0;

Local

Similarity

28.2%; 98.9%;

Score 261.2; DB 8 Pred. No. 5.7e-55; Mismatches

DB 8;

Length

88356; 0;

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Gaps 60

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CGQAFGAKKYHHLGVYWQRSWIYVLFFCCVLLLPTY!FTPVLKFLGOPDDIAELSGVV
AIWVIPLHFAFTLSFPLQRFLQCDLYNWTMAAAVALLYUCWLFVDLEKLGARGK
AVWIPLHFAFTLSFPLQRFLQCOPLTWTGLSSEALTGLWEELKLSASSGVWLCLEN
WYYRILIIMTGNLQNARIAVDSLSICMAINGEMMIPLAFFAGTGVRVANELGAGNGK
GARFATTVSVTQSLIIGLFFWVLIMLINQIAWIESSSVAVLDAVNKLSLLLAFTVLL
NSVQPVLSGVAVGSGWQSYVAYINLGCYYCIGVPLGFLMGWGFKLGVMGIWGGMIFGG
TAVQTMILSFITMRCDWEKEAQKASARINKWSNTIK"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        complement(join(35140...35190,35286.
35671...35909,36671...36727,36968....
37601...37888.37976...38251))
/note="emb|CABB9401.1
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GTVALBDIRKYQKSTEILIRKLPFQRLVREIAQDFKTDLRFQSSAVAALQEAAEAYLV
GLFEDTNLCAIHAKRVTIMPKEIQLARRIRGERARGE"
                                                                                                                                                                                                                                                                                                                                                                                                                              strong similarity to unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   gene_id:MNA5.11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RSKYLIADFWYLVSKLKDM"
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IAEVLGITPNIKEKNEDKRLETQRVSSYPMDCILKQIDFLVELFEHISDRPKAPQSKL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /evidence=not_experimental
/protein_id="BAB11559.1"
/db_xref="G1:9759617"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              similar to unknown protein"
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GLFEDTNLCAIHAKRVTIMPKDIQLARRIRGERA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /product="histone H3"
/protein_id="BAB11558.1"
/db_xref="GI:9759616"
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NMYCNGRKVGFAIKREPSKSELAALKVLTPVAEGAGVVNGEEINREKSDHMMYLRASF
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PSCYCTIVDPNDSQEDKLSHRQIKPRTSSASSTATNSTFTGTIFGFRRGKVNFCIQAT
                                                                                                                                                                                                                                                                                                                                                                                                   codon_start=1/
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        translation="MARTKQTARKSTGGKAPRKQLATKAARKSAPATGGVKKPHRFRP/
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/db_xref="GI:9759615"
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                                                                                                              Query Match
Best Local Similarity
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                                 603
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TGATTACATCAAGAGACTTAGAAGTGGAGATTTGGATTTGAATGTTGGAAGAAGAGATGC 242
                                                                                                440;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GCCCTCAATTGGATTTGGAAGGTCTG
                                GGCAAATCATGAGTGTTTGGCTTCCTTGTTTGACAATGAAAGACAACATTTTCTGGGTCT 662
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nucleotide sequence of a cDNA encoding a D-type cyclin from a photoautotrophic cell suspension culture of Chenopodium rubium Plant Physiol. In press
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Direct Submission
Submitted (18-DEC-1996) A. Renz, Lehrstuhl i
Pflanzenphysiologie, Universitaet Bayreuth,
95447 Bayreuth, FRG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Caryophyllidae; Caryophyllales; Chenopodiaceae; Chenopodium.
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                                                                                                Conservative
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LRNFDDFTLILLIIKENNEFALISGFFVANHECLASLEDNERQHFLGLDYLKRERNG
DLDLGARNLYDDWIKVGSHYNFGPLCVYLSWYLDRELSAYELPGKAMMMQLLGYGE
LSLAAKVDETDVPLILDLQVSESKFVFEAKTIQRMELLVLSTLKWRMQSVTPFSSTIDY
ELYKLSGDKMPSKSLLFQAIQLILSTIKGIDLMEFRESEIAAAVAISVTQQTQIVEFT
DKAFSFLTDHVEKERLMKCVEIMHDLRMSSRSNGALASTSVPQSPIGVLDASACLSYK
SDDTSTTPSGSCGNSAHSSPASAPPKRKLDFTSQIS"
283 c 308 g 552 t 2 others
                                                                                                                                                                                                                                                                                                                       /product="cyclin-D like protein"
/protein_id="CAA71244.1"
/db_xref="SPTREMBL:P93103"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Chenopodium rubrum"
/db_xref="taxon:3560"
/dev_stage="7 day old culture"
/clone_lib="lambda uniZAP-XR"
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Pred. No. 2.5e-54;
0; Mismatches 238;
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Sequence
A85077
                                                                                                                               MUTTAY,J.A.
PLANTS WITH MODIFIED GROWTH
PATHON: WO 9842851-A 21 01-OCT-1998;
MURRAY JAMES AUGUSTUS HENRY (GB); UN
                                                                                                                                                                                            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade; Panicoideae; Andropogoneae; Zea.
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                                                               /organism="Zea mays"
/db_xref="taxon:4577"
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Score 193.4; DB 6;
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                  Molecular Genetics Dep. E-mail: michael.beyan@bbsrc.ac.uk
Information on performance
annotation of this entry and
                                                                        Submitted (28-APR-2000) MIPS, at the Max-Planck-Institut fuer Biochemie, Am Klopferspitz 18a, D-82152 Martinsried, FRG, E-m. lemcke@mips.biochem.mpg.de,mayer@mips.biochem.mpg.de Project Coordinator: Mike Bevan, Molecular Genetics Department, Cambr.
                                                                                                                                                                                                                                                                                                                                                                                              project)
AL353995
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Arabidopsis sequencing, project.
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       on performance of analysis and a more detailed of this entry and other sequences of chromosomes 3,
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clone F12B17 (ESSA
                                                                                                                                                                                                                                    Lemcke, K. and
                                                           7UJ Norwich,
                                                                          Cambridge
                                                                                                            E-mail:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /gene="F12B17_10"
/number=2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GLWRCAICTYDNVETMEVCDICGVLRIEVAGNOSINKNTAVRVVSLFAIVVLQRRYSD
SSFSTYVAPFKEDAPSPDDLVSNGLTSSKTGPKGSGDASMRQKEKQDSVEQKPLKKGG
DSSETSSRGRHDKLDKGGAGGIKSGKSLFKARADMSNETSSSKYMETSESLTGTMN
KMSLIGETENSSDIKIRGPKSOSKHRPEEMMLLDKESDALSQLILAIVGHVDSGKSTL
SGRLLHLLGRISQKQMHKYEKEAKLQGKGSFAYAWALDESAEERERGITMTVAVAYFN
SKRHHVVLLDSSPGHKOPVPNMIAGATQADAATLVIDASVGAPEAGFDNLKGQTREHAR
VLRGFGVEQVIVAINKMDIVGYSKERFDLIKGTSLQSCRRKDSSLTMIPLSAMEN
QNLVAAPSDNRLSSWYQGPCLLDAVDSVKSPDRDVSRFLDAVRSTSQGQVSAC
GKLEAGAVRPGSKVMVMPSGDQGTIRSLERDSQACTIARAGDNVALALQGIDANQVMA
GDVLCHPDFPYSVATHLELMYLVLBGATPILLGSQLEFHVHHAKEAATVVKLVAMLDP
     complement(2926.
/number=7
                                                                        complement(2537
                                                                                                                                                                                                                               complement(1772.
/gene="F12B17_10"
                                                                                                                                                                                                                                                                                                                  complement(1493.
/gene="F12B17_10"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              complement(join(447. .575,662. 1772. .2259,2348. .2458,2537. .4198. .4309,5607. .5927))
//gene="F12B17_10"
                                                                                          /number=6
                                                                                                           complement(2459.
                                                                                                                                                             complement(2348
                                                                                                                                                                                            complement(2260.
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//gene="F12B17_10"
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                                                        /gene="F12B17_10"
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/protein_id="CAB89379.1"
/db_xref="GI:7671439"
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/number=1
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/chromosome="5"
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/variety="Columbia"
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/db_xref="G1:7671441"
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/translation="MSISVMANSHLNQDYASASPTPQEKGRTGRYAGGAVRALDIRVI
TVGKRRSEGVELLVDBYKIKLKPYCSFEDSLYRSNFRNAQDVRAQVEDEEVAMMKLIG
SDDWYLDERGRIDIDSEQMAELLGDAGNSGASRISFCIGGAYGHGTQVRKRANVTIR
LSSMVLNHQIALVVLMEQLYRSWTILKGQNYHH"
8322. 8417
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complement(5589. 5927)
/gene="F12B17_20"
/gene="F12B17_20"
/gene="strong similarity to FPF1 protein, Arabidopsis thaliana, EMBL:ATFPF1"
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/gene="F12B17_30"

/oin(8246. .8321,8418. .8449,8529. .6

8906. .8983,9136. .9281,9356. .9395)

/gene="F12B17_30"

/note="similarity to predicted proteing the state of the st
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/protein_id="CABB9380,1"
/db_xref="G1:7671440"
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/gene="F12B17_20"
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/gene="F12B17_20"
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/gene="F12B17_10"
/number=8
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/gene="F12B17_20"
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/gene="F12B17_30"
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                                                                                           /gene="F12B17_30'
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ORGANISM
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TITLE
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TGTTGAACAAATTGAAATGGAGATTGAGAGCAATAAÇTCCATGCTCATACATAAGATATT 565
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TCCTGAGTAAGATCAATGGCTATGATCAAGAACCACATAGCAGATTGGTAACTAGATCAC 83415
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                                                                                                                                                                                                                                                                                                                     common tobacco.

Nicotiana tabacum

Licotiana tabac
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Sequence 2 from Patent W09842851.
A85058
                                                                                                                                                         PLANTS WITH MODIFIED GROWTH
PATENT: WO 9842851-A 2 01-OCT-1998;
MURRAY JAMES AUGUSTUS HEBRRY (GB); U
Location/Qualifiers
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                                                                                                                                                                                                                                                                                          Murray,J.A.
                                  537
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complement(9841. .11343)
/gene="F12B17_40"
/gene="F12B17_40"
/number=1
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8906. .8983
/gene="F12B17_30"
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/gene="F12B17_40"
complement(9841. .11343)
/gene="F12B17_40"
/gene="F12B17_40"
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tuberosus, EMBL:HTCYP81L"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9282. .9355
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                       /organism="Nicotiana tabacum"
/db_xref="taxon:4097"
281 c 293 g 568 t
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Pred. No. 1.2e-26;
0; Mismatches 38
                                                                                                                                                                                              VIND
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                                                                                                                                                                                              CAMBRIDGE TECH: (GB)
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REFERENCE
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ORGANISM
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NTA011893
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ACTGAAGTTCCAATGTTGATAGATCTTCAGGTTGGAGATCCTCAGTTTGTGTTTTGAGGCT 477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GTTTTAGCCATAAATTACTTTGACAGGTTTCTGACTAGTCTTCATTATCAGAAAGATAAA 612
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CACTGGGAATTTCTTAGAAGATGTGAAAATCTCCTCCTCTCTATTATGGCTGATTGTAGA 912
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TGCTTAGCAATGAACTACTTGGATCGATCTTATCGGTTCATGATTTTGCCTAGTGGCAAA 357
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          309;
                                                                                    Direct Submission
Submitted (07-OCT-1998) Murray J.A.H.,
University of Cambridge, Tennis Court
2 (bases 1 to 1679)
                                                                                                                                                                       Nicotiana tabacum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Asgnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids I; Solanales; Solanaceae; Nicotiana.

1 (bases 1 to 1679)
levels of transcripts in tobacco bright yellow-2 cells
                           Murray,J.A.

Distinct cyclin D genes show mitotic accumulation or constant
                                                                Sorrell,D.A.,
                                                                                                                                                                                                                                                                                             CycD3.1 gene; cyclin D3.1 protein
                                                                                                                                                               Murray,J.A.H.
                                                                                                                                                                                                                                                                           common tobacco
                                                                                                                                                                                                                                                                                                                                    AJ01189:
                                                                                                                                                                                                                                                                                                                AJ011893.1 GI:4160299
                                                                                                                                                                                                                                                                                                                                                Nicotiana tabacum mRNA for cyclin D3.1 protein (CycD3.1)
                                                                                                                                                                                                                                                                                                                                                                       NTA011893
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                                                                                                                                                                                                                                                                                                                                                                       1679
                                                                Combettes, B., Chaubet-Gigot, N., Gigot, C.
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Pred. No. 1.2e-21;
0; Mismatches 302;
                                                                                                                                                                                                                                                                                                                                                                       mRNA
                                                                                                    Institute of Biotechnology, Road, Cambridge, CB2 1QT, UK
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GACTTTTTGGAGTTTAGACCTTCTGAAGCTGCTGCTGCTGTGGCACTTTCTGTTTCTGGA
                                                                                                                                                                                                                                                                                                           ACTGAAGTTCCAATGTTGATAGATCTTCAGGTTTGGAGATCCTCAGTTTTGTGTTTTGAGGCT
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                                                         ATAACTCCATGCTCATACATAAGATATTTCCTGAGAAAGATGAGTAAATGTGATCAAGAA
                                                                                                                                                                                                                               AAATCAGTCCAAAGAATGGAGCTTTTTGGTGTTGAACAAATTGAAATTGAGAGTTGAGAGCA
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                                                                                             CCATCCAACACATTGATATCTAGATCATTACAAGTGATAGCCAGCACAACCAAAGGTATT
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1120. 1218
/gene="CycD3.1"
/note="Potential PEST s
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EVTTTTTTTTTTRNSLLPLLLEQDLTWEDEELLSLESKEKETHGWENSFQDDSLLCSA
RVDSVEWILKVNGYYGFSALTAVLAINYFDREITLSLLFSKEKETHGWENSFQDDSLLCSA
KVEETQVFLLLDFQVEDAKYYEAKTIQRMELLVLSSLKWRMMPVTPLSFLDHIIRLA
GLRNNIHWEFLRRCENLLLSIMADCREVRYMPSVLATAIMLHVIHQVEPCNSVDYQNQ
LLGVLKINKEKVNNCFELISECSKPISHKRKYENPSHSPSGVIDPIYSSESSNDSWD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /product="cyclin D3.1
/protein_id="CAA09853
/db_xref="GI:4160300"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /gene="CycD3.1"
181. .1302
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /gene="CycD3.1"
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/cell_line="Bright Yellow 2 (BY-2)"
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                                                                                                                                                 Local Similarity
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                                                        AGAGATGAGGCTGTTGAATGGATGTTTAAGGTCATTGGGTACTATTCTTTTTCTGCTCTC 427
                                                                                           AGAAGAGATGCCCTCAATTGGATTTGGAAGGCTTGTGAAGTACACCAGTTTGGACCATTG 291
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AJ250397
AJ250397.1 GI:6448481
CYCD3a gene; CYClin D3a.
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The expression of D-cyclin genes define distinct developmental zones in Antirrhinum apical meristems and is locally regulated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids I; Lamiales; Veronicaceae; Antirrhinum.

1 (bases 1 to 1140)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Centre,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Unpublished
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                                                                                                                                                                                                                                               332
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                                                                                                                                                                                                                                                                              /product="cyclin d3a"
/protein_id="cyclin d3a"
/protein_id="cab61222.1"
/db_xref="G1:6448482"
/translation="MYQQNSPSLCFDALYCEEBQNWDNGEIINDCFIEBQEPFSDLLK
/translation="MYQQNSPSLCFDALYCEEBQNWDNGEIINDCFIEBQEPFSDLLK
HDLLCGVDDDDDDKEELSSLLCKEQEYELYRVLEDNPSLAKARDEAVEWMFKVIGYYS
FSALTAVIAVNYLDRFLCTFOFQQDKFWMYQLAVAGLISLAKVEETQVPLLLDLQVE
ESALTAVIAVNYLDRFLCTFOFQQDKFWMYQLAVAGLISLAKKSHLCKEFINRCE
ESKYTYPESKTIQRMELLVLSTLKMKMNPVTPISFLEYINFLGINKDKVEECC
LLSLITDCRFWCHLPSALATATMLYVLSSLEPCIGVEYQDQLLNILGINKDKVEECC
LLSLITDCRFWCHLPSALATATMLYVLSSLEPCIGVEYQDQLLNILGINKDKVEECC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /gene="
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Antirrhinum majus"
/db_xref="taxon:4151"
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GAGGATGAACCCAGTGACAATCTCATTTCTTGATCACATTGTAAGAAGGCTTGGATT
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                                                                        TGTGTTTGAGGCTAAATCAGTCCAAAGAATGGAGCTTTTGGTGTTTGAACAAATTGAAATTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Murray, J.A.
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/db_xref="taxon:4233"
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AAGAAACTGAAGTTCCAATGTTGATAGATCTTCAGGTTGGAGATCCTCAGTTTGTGTTTTG
                                                                 GCAAAGGTTGGATATTGCAGTTGTTGGCTGGCTTGTTTATCATTGGCAGCCAAAATTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (03-JUN-1998) to the DDBJ/EMBL/GenBank databases. M Sekine, Nara Institute of Science and Technology, Graduate Sc of Biological Sciences; Takayama 8916-5, Ikoma, Nara 630-0101 Japan (E-mail:sekine@bs.aist-nara.ac.jp, Tel:+81-743-72-5482, Fax:+81-743-72-5469)
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/db_xref="GI:4586801"
/translation="McJQHNBEHQDQTQSFILDALYCEEERWEETIEDEILEKEATLP
LPLPLLEQDLFWEDEELLSLFTKEKETISNFETIKTDPLLCLSRKEAYKWILKVNAHY
GFSTFTAILAINYFDRFLSSLHFQKDKFWMIQLVAVTCLSLAAKVEETQVPLLLDFOV
EDAKYVFEAKTIQRWELLVLSSLKWRWNPVTPLSFVDHIIRRLGLKSHIHWEFLKQCE
RILLIVIADCRFLSYMPSVLATATMLHVIHQVEPCNAADYQNQLLEVLNISKEKVNDC
YELITEVSYNSISHKRKYESPINSPSAVIDTFYSSENSNESWDLQTSSSIPSTYSPRD
QFLPLFKKSRVQEQQMRLTSLSRVFVDYAVGSPR"
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Location/Qualifiers
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1 257 c
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N. tabacum CYCD3;
H.tuberosus CYCD3
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12 123 13,3 1788 19 AAV33887 H. tuberosus 13 118.4 12.8 1431 19 AAV33886 N. tabacum C 14 116 12.5 1311 21 AAC4023 Arabidopsis 15 111.2 12.0 1337 21 AAC42423 Arabidopsis 16 104.2 11.2 1358 21 AAC31463 Arabidopsis 17 104.2 11.0 936 22 AAF58252 Oligonucleot 19 102.2 11.0 936 22 AAF58254 Oligonucleot 20 102.2 11.0 936 22 AAF58254 Oligonucleot 21 102.2 11.0 936 22 AAF58254 Oligonucleot 21 102.2 11.0 936 22 AAF58259 Oligonucleot 22 102.2 11.0 936 22 AAF58259 Oligonucleot 23 102.2	Soybean cyclin	AAZ19958		2259	0	97.8	30	
12 123.2 13.3 1788 19 AAV33887 H. tuberosus 13 118.4 12.8 1431 19 AAV33886 N. tabacum C 14 116 12.5 1311 21 AAC40202 Arabidopsis 15 111.2 12.0 1337 21 AAC42423 Arabidopsis 16 104.2 11.2 1356 21 AAC31463 Arabidopsis 17 104.2 11.2 1358 21 AAC31433 Arabidopsis 18 102.2 11.0 936 22 AAF58252 Oligonucleot 19 102.2 11.0 936 22 AAF58253 Oligonucleot 20 102.2 11.0 936 22 AAF58254 Oligonucleot 21 102.2 11.0 936 22 AAF58252 Oligonucleot 21 102.2 11.0 936 22 AAF58252 Oligonucleot 23 102.2	Oligonucleotide	AAF58255		938	0	99.6	29	
12 13.3 178B 19 AAV33887 N. tuberosus 13 118.4 12.8 1431 19 AAV33886 N. tabacum C 14 116 12.5 131 21 AAC40202 Arabidopsis 15 111.2 12.0 1337 21 AAC42423 Arabidopsis 16 104.2 11.2 1356 21 AAC51463 Arabidopsis 17 104.2 11.2 1358 21 AAC51463 Arabidopsis 18 102.2 11.0 936 22 AAF58252 Oligonucleot 19 102.2 11.0 936 22 AAF58253 Oligonucleot 20 102.2 11.0 936 22 AAF58259 Oligonucleot 21 102.2 11.0 936 22 AAF58259 Oligonucleot 21 102.2 11.0 936 22 AAF58259 Oligonucleot 23 102.2 11.0	Oligonucleotide	AAF58262		936	0	99.6	28	
12 123.2 13.3 1788 19 AAV33887 H.tuberosus 13 118.4 12.8 1431 19 AAV33886 N. tabacum C 14 116 12.5 1311 21 AAC40202 Arabidopsis 15 111.2 12.0 1337 21 AAC42423 Arabidopsis 16 104.2 11.2 1356 21 AAC31463 Arabidopsis 17 104.2 11.2 1358 21 AAC33723 Arabidopsis 18 102.2 11.0 936 22 AAF58254 Oligonucleot 19 102.2 11.0 936 22 AAF58254 Oligonucleot 20 102.2 11.0 936 22 AAF58259 Oligonucleot 21 102.2 11.0 936 22 AAF58259 Oligonucleot 21 102.2 11.0 936 22 AAF58255 Oligonucleot 22 102.2 11.0 936 22 AAF58259 Oligonucleot 23 102.2 11.0 936 22 AAF58255 Oligonucleot 24 99.6 10.7 936 22 AAF5825<	Oligonucleotide	AAF58259		936	10.7	99.6	27	
12 123 13,3 1788 19 AAV33887 N. tabacoum C 13 118.4 12.8 1431 19 AAV33886 N. tabacoum C 14 116 12.5 1311 21 AAC40203 Arabidopsis 15 111.2 12.0 1337 21 AAC42423 Arabidopsis 16 104.2 11.2 1356 21 AAC31463 Arabidopsis 17 104.2 11.2 1358 21 AAC3733 Arabidopsis 18 102.2 11.0 936 22 AAF58252 Oligonucleot 19 102.2 11.0 936 22 AAF58254 Oligonucleot 20 102.2 11.0 936 22 AAF58259 Oligonucleot 21 102.2 11.0 936 22 AAF58250 Oligonucleot 21 102.2 11.0 936 22 AAF58250 Oligonucleot 23 102.2	Oligonucleotide	AAF58257		936	10.7	99.6	26	
12 123.2 13.3 1788 19 AAV33887 H. tuberosus 13 118.4 12.8 1431 19 AAV33886 N. tabacum C N. tabacum C Arabidopsis	Oligonucleotide	AAF58254	22	936	10.7	99.6	25	
12 123.2 13.3 1788 19 AAV33887 H.tuberosus 13 118.4 12.8 1431 12 AAV33886 N. tabacum C 14 116 12.5 1311 21 AAC40202 Arabidopsis 15 111.2 12.0 1337 21 AAC42423 Arabidopsis 16 104.2 11.2 1356 21 AAC51463 Arabidopsis 17 104.2 11.2 1358 21 AAC53723 Arabidopsis 18 102.2 11.0 936 22 AAF58254 Oligonucleot 19 102.2 11.0 936 22 AAF58257 Oligonucleot 20 102.2 11.0 936 22 AAF58250 Oligonucleot 21 102.2 11.0 936 22 AAF58250 Oligonucleot 21 102.2 11.0 936 22 AAF58250 Oligonucleot 22 102.2 11.0 936 22 AAF58250 Oligonucleot 23 102.2 11.0 936 22 AAF5825 Oligonucleot 23 102.2 11.0 936 22 AAF5825<	Oligonucleotide	AAF58252	22	936		99.6	24	
12 123.2 13.3 1788 19 AAV33887 H.tuberosus 13 118.4 12.8 1431 19 AAV33886 N. tabacum C 14 116 12.5 1311 21 AAC40202 Arabidopsis 15 111.2 12.0 1337 21 AAC42423 Arabidopsis 16 104.2 11.2 1356 21 AAC31723 Arabidopsis 17 104.2 11.2 1358 21 AAC33723 Arabidopsis 18 102.2 11.0 936 22 AAF58254 Oligonucleot 19 102.2 11.0 936 22 AAF58257 Oligonucleot 20 102.2 11.0 936 22 AAF58259 Oligonucleot 21 102.2 11.0 936 22 AAF58250 Oligonucleot	Oligonucleotide	AAF58255		938		102.2	23	C
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12 123.2 13.3 1788 19 AAV33887 H. tuberosus 13 118.4 12.8 1431 19 AAV33886 N. tabacum C 14 116 12.5 1311 21 AAC40202 Arabidopsis 1.5 111.2 12.0 1337 21 AAC42423 Arabidopsis 1.6 104.2 11.2 1356 21 AAC51463 Arabidopsis 1.7 104.2 11.2 1358 21 AAC33723 Arabidopsis 1.8 102.2 11.0 936 22 AAF58252 Oligonucleot 19 102.2 11.0 936 22 AAF58257 Oligonucleot 20 102.2 11.0 936 22 AAF58257 Oligonucleot	Oligonucleotide	AAF58259		936	-	102.2	21	C
12 123.2 13.3 1788 19 AAV33887 H.tuberosus 13 118.4 12.8 1431 12 AAV403886 N. tabacum C 14 116 12.5 1311 21 AAC40202 Arabidopsis 15 111.2 12.0 1337 21 AAC42423 Arabidopsis 16 104.2 11.2 1356 21 AAC33723 Arabidopsis 17 104.2 11.2 1358 21 AAF58552 Oligonucleot 18 102.2 11.0 936 22 AAF58553 Oligonucleot 19 102.2 11.0 936 22 AAF585254 Oligonucleot	Oligonucleotide	AAF58257		936	1	102.2	20	C
12 123.2 13.3 1788 19 AAV33887 H. tuberosus 13 118.4 12.8 1431 19 AAV33886 N. tabacum C 14 116 12.5 1311 21 AAC40202 Arabidopsis 1.5 111.2 12.0 1337 21 AAC42423 Arabidopsis 16 104.2 11.2 1356 21 AAC31723 Arabidopsis 17 104.2 11.2 1358 21 AAC33723 Arabidopsis 18 102.2 11.0 936 22 AAF58252 Oligonucleot	Oligonucleotide	AAF58254		. 936	11.0	102.2	19	C
123.2 13.3 1788 19 AAV33887 H.tuberosus 118.4 12.8 1431 19 AAV33886 N. tabacum C 116 12.5 1311 21 AAC40202 Arabidopsis 111.2 12.0 1337 21 AAC4423 Arabidopsis 104.2 11.2 1356 21 AAC33723 Arabidopsis Arabidopsis	Oligonucleotide	AAF58252		936	11.0	102.2	18	C
123.2 13.3 1788 19 AAV33887 H.tuberosus 118.4 12.8 1431 19 AAV33886 N. tabacum C 116 12.5 1311 21 AAC42423 Arabidopsis 111.2 12.0 1337 21 AAC42423 Arabidopsis 104.2 11.2 1356 21 AAC51463 Arabidopsis		AAC33723		1358	11.2	104.2	17	
123.2 13.3 1788 19 AAV33887 H.tuberosus 118.4 12.8 1431 19 AAV33886 N. tabacum C 116 12.5 1311 21 AAC40202 Arabidopsis 111.2 12.0 1337 21 AAC42423 Arabidopsis		AAC51463		1356		104.2	16	
123.2 13.3 1788 19 AAV33887 H.tuberosus 118.4 12.8 1431 19 AAV33886 N. tabacum C 116 12.5 1311 21 AAC40202 Arabidopsis		AAC42423	21	1337		111.2	15	
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123.2 13.3 1788 19 AAV33887 H.tuberosus	N. tabacum CYCI	3388	19	1431		8	13	
		338	19	1788	13.3	ω.	12	

ALIGNMENTS

RESULT AAX36897

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AAX36897 standard; cDNA; 927

ВP

Mitogenic cyclin CYCD4 coding sequence.

16-JUL-1999 (first entry)

AAX36897;

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PXX DRX PAX PR
                                                                                                                                                                       Mitogenic cyclin; CYCD4; modulator; plant cell cycle; growth inhibitor; plant cell division; cell growth; regulator; cell proliferation; growth regulator; herbicide; cell division progression; ds.
Claim 1; Page 47-49; 57pp; English.
                      DNA sequence encoding a mitogenic cyclin
                                                P-PSDB; AAY14071.
                                                          WPI; 1999-312966/26.
                                                                                 De Almeide J, De Veylder L,
                                                                                                                                  24-OCT-1997;
                                                                                                                                                         23-OCT-1998;
                                                                                                                                                                                   06-MAY-1999
                                                                                                                                                                                                         W09922002-A1
                                                                                                                                                                                                                                Arabidopsis thaliana.
                                                                                                          (CROP-) CROPDESIGN NV.
                                                                                                                                 97EP-0203303
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Query Match
Best Local Sim
Matches 927;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This sequence encodes the mitogenic cyclin, CYCD4, of the invention. The DNA sequence, vectors containing it, protein encoded by it, or antibodies recognising the protein can be used for modulating plant cell cycle, plant cell division and/or growth, for influencing the activity of mitogenic cyclin in a plant cell, as positive or negative regulator of cell proliferation, for modifying the growth inhibition caused by environmental stress conditions, or for use in a screening method for the dentification of inhibitors or activators of cell cycle proteins. A compound which is an activator or inhibitor of the mitogenic cyclin can be used as a growth regulator and/or herbicide. The proteins can also be used to influence cell division progression in yeast, mammals and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 927 BP;
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 721
                                    721
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TCAGTCCAAAGAATGGAGCTTTTGGTGTTGAACAAATTGAAATGGAGAGTTGAGAGCAATA
                                                                                                                                                                                                                                                                                                                                                                                 GAAGTTCCAATGTTGATAGATCTTCAGGTTGGAGATCCTCAGTTTGTGTTTTGAGGCTAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                         TGGATATTGCAGTTGTTGGCCTGTGGCTTTATCATTGGCAGCAAAATTGAAGAAACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATGGCAGAGGAAAATCTAGAACTGAGTCTTTTATGTACAGAGAGACAACGTTGATGAG
TCCAACACATTGATATCTAGATCATTACAAGTGATAGCCAGCACAACCAAAGGTATTGAC
                                                                                                                                                                                                                                      ACTCCATGCTCATACATAAGATATTTCCTGAGAAAGATGAGTAAATGTGATCAAGAACCA
                                                                                                                                                                                                                                                                                                                                                               gaagttccaatgttgatagatcttcaggttggagatcctcagtttgtgttttgaggctaaa
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.0%; Pred. No. 9. |
0; Mismatches
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1.8e-253;
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30-APR-1999
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06-MAY-1999
07-MAY-1999
14-MAY-1999
18-MAY-1999
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                                                                                                                                                                                                                                                                                    23-MAR-1999;
25-MAR-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                Hybridisation assay; genetic mapping; gene expressio protein identification; signal transduction pathway; metabolic pathway; promoter; termination sequence; s
                                                                                                                                                                                                                                                                                                                                                                                                                                Arabidopsis thaliana
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on; signal transduction pathway;
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XX AAV
XX AV
DT 25-1
XX D-t.
KW CDC
KW CCO
XX Nico
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PN WO91
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                                             26-MAR-1997;
                                                                  24-MAR-1998;
                                                                                                                 W09842851-A1
                                                                                                                                      Nicotiana tabacum
                                                                                                                                                                 D-type cyclin; growtn; אינמור, ערבו ער CDC; Rb; retinoblastoma; germination;
                                                                                                                                                                                                                                                                                                                                                                                 1084
                      (UYCA-) UNIV
                                                                                                                                                                                                                                 25-JAN-1999
                                                                                                                                                                                                                                                                            AAV33884 standard;
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                                                                                                                                                                                                       tabacum CYCD2;1 gene.
                                                                                                                                                                                                                                                                                                                                                                            GAGAGAGTGAAGATAGGGGAAATGATAGAGAGTGATGGCTCAGACTTATGTTCACAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 development;
                                                                                                                                                                                                                                                                                                                                              TCTTCTTCTTATACACATCTTTCTTAA 927
                                                                                                                                                                                                                                                                                                                                                                                                                          gagagagtgaagataggggaaatgatagagagtgatggctcagacttatttcacaa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TTTTTGGAGTTTAGACCTTCTGAAGCTGCTGCTGCTGTGGCACTTTCTGTTTTCTGGAGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TCCAACACATTGATATCTAGATCATTACAAGTGATAGCCAGCACAAAGGTATTGAC
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                                                                                                                                                                                 cyclin; growth; plant; cell-division control;
                     CAMBRIDGE TECH SERVICES LTD.
                                                                                                                                                                                                                               (first entry)
                                            97EP-0302096
                                                                    98WO-EP01701
                                                                                                                                                             ds
                                                                                                                                                                                                                                                                            cDNA to
                                                                                                                                                                                                                                                                           mRNA;
                                                                                                                                                                       flowering; seed;
                                                                                                                                                                       phosphorylation;
d; fruit;
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Claim
                                                                                                                                                    Regulating growth and structure of plants by modulating protein controls cell division - specifically a D-type cyclin, and relat chimeric genes and transformed cells and plants, used to alter
                                                                                                                                             growth rate, flowering,
                                                                                                                                                                                          1998-532012/45
                                                                                                                             14;
                                                                                                                          p52-53; 75pp; English
                                                                                                                                             seed production etc.
                                                                                                                                                      yclin, and related used to alter
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This sequence represents the CYCD2;1 cDNA from Nicotiana tabacum which encodes a D-type cyclin. The sequence can be used to alter the growth characteristics or architecture of plants by altering the (functional) level in the plant cells of a cell-division controlling protein that can bind to, or phosphorylate, an Rb-like protein, such as a D-type cyclin. Modulation of the cyclin gene is used to increase or decrease the growth rate, provide faster germination, reduce time to flowering, increase mumber of flowers, seeds or fruits per plant, increase root development, number of flowers, seeds or fruits per plant, increase root developme reduce height and to delay flowering in a range of plants, e.g. legum grasses, maize, oilseed rape, wheat, tomato, rice, barley, sunflower, carnation, chrysanthemum, rose, tulip, etc.

Sequence 1284 ВP; 415 A; 179 Ç 261 G; 429 T; 0 other;

Query Match Best Local

Local Similarity

32.6%;

Score 302.2; DI Pred. No. 1e-75;

DB 19;

Length

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                           AGAGTACACTTTGACAACTCTTCCTTCTCCTCTCTTTTTCTCACTACTTCAAAAAGGAGAGA 786
                                                                                                                                                                                                                                            CAAAGAATGGAGCTTTTGGTGTTGAACAAATTGAAATGGAGATTGAGAGCAATAACTCCA 546
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                                                                                                                           ACATTGATATCTAGATCATTACAAGTGATAGCCAGCACAACCAAAGGTATTGACTTTTTG
                                                                                                                                                                                  TGCTCATACATAAGATATTTCCTGAGAAAGATGAGTAAATGTGATCAAGAACCATCCAAC
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                                                    gaattcaggtcttctgaaattgcagcatcagtggcaatgtctgtttcaggggaaatacaa
                                                                                                             ccgttgatttctggatcaatgcaactgatattaagcataataagaagtattgatttcttg
                                                                                                                                                                    tacacattcatagattattttatgagaaagatg---aatggtgatcaaatcccatctcgg
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TACATCAAGAGACTTAGAAGTGGGAGATTTGGGATTTGGAATGTTGGAAGAGAGAGAGATGCCCTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             tatgtcgagagttgagaagtggagatttggatttgagtgt---gagaaaagaggctctt
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-ggcaatgccttgcttcttcatacacttagacaagggtaga
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787

1016 gtgcagaagtgtgttgaactgat 1038

GTGAAGAAGATAGGGGAAATGAT

809

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RESULT
AAZ94582
ID AAZ9
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        recombinant expression cassettes (including incycl in sense or antisense orientation), host cells, transgenic plants (especially corn, sorghum, sunflower, safflower, wheat, rice, alfalfa or coilseed Brassica) and antibody compositions. A claimed method of modulating the level of Cycl protein in a cell comprises transforming the cell with a recombinant expression cassette comprising a Cycl polynucleotide linked to a promoter, and growing the cell for a time sufficient to induce expression of the cycl protein in the cell. The Cycl protein is present in an amount sufficient to modulate (increase or decrease) the cycl protein to alter cell division, increase the number of cells increase the growth rate, increase crop yield, alter plant height or size, enhance or inhibit organ (seed, root, shoot, ear, tassel, stalk, pollen, stamen) growth, produce organ ablation, compositive selection, increase plant regeneration, plants, enhance embryogenic response, increase callus induction, provide consitive selection; increase plant regeneration, alter the time constitution of the const
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present sequence is that of an isoform of the maize ZmCycD gene that encodes cyclin D (Cych, see AA79322), a protein necessary for progression from G1 into S phase. The encoded protein binds to CDK4, and the active CycD-CDK4 hyperphosphorylates retinoblastoma. associated protein, releasing the E2F transcription factor which activates DNA synthesis. The invention provides maize CycD polynucleotides (see AA294581-84) and polypeptides (see AAY79321-24) that are involved in cell cycle regulation. Also provided are
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Novel polynucleotides encoding related proteins and antisense regulation -
dehydration, heat or cold, increase the number of pods per plant, increase the number of seeds per pod or ear, alter the lag time i seed development, provide hormone-independent cell growth, or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 1; Page 120-121; 134pp; English
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P-PSDB; AAY79322.
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RNA useful for control (
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RESULT AAV33889 ID AAV3

standard;

cDNA to

mRNA; 1846

6

AAV33889; AAV33889

Maize CYCD2

gene

25-JAN-1999

(first entry)

D-type cyclin; growth; plant; CDC; Rb; retinoblastoma; germi

germination;

cell-division control; ination; flowering; see

seed;

phosphorylation; d; fruit;

root development; ds

Zea mays

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     increase the growth rate of cells in bioreactors. The level of CycD protein in the cells is transiently modulated by introducing CycD RNA or CycD polypeptides. CycD polypucleotides can be used to identify CycD interacting proteins. All claimed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 1077 BP; 228 A; 265 C; 308 G; 276 T; 0 other;
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                                                                        TGAAGCTGCTGCTGTGTGGCACTTTCTGTTTCTGGAGAATTGCAGAGAGTACACTTTGA
                                                                                                                                 ATCATTACAAGTGATAGCCAGCACAACCAAAGGTATTGACTTTTTGGAGTTTTAGACCTTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    acggcatggggacctggatttggtcgccgtcaggaaggacgccatcgattggatttggaa
gagagctgc
                             CAACTCTTC
                                                                                                                                                                                           ATATTTCCTGAGAAAGATGAGTAAATGTGATCAAGAACCATCCAACACATTGATATCTAG
                                                                                                                                                                                                                                                    TCTTCAGGTTGGAGATCCTCAGTTTGTTTTGAGGCTAAATCAGTCCAAAGAATGGAGCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GATGGTGGAGAAGGAGAAGCAGCATTTGCCAAGTGATGATTACATCAAGAGACT-----
                                                        cgagattgctgccagtgttgcacttgctgctatcggcgaatgcaggagttctgtaattga
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                                                                                                                                                                                                                                      tttgcaggtagcggaggcaaagtttgtttttgagggaaggaccataaaaaggatggagct
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Pred. No. 6.3e-45;
0; Mismatches 236
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This sequence represents the CYCD1:1 cDNA from Zea mays which encodes a D-type cyclin. The sequence can be used to alter the growth characteristics or architecture of plants by altering the (functional) level in the plant cells of a cell-division controlling protein that can bind to, or phosphorylate, an Rb-like protein, such as a D-type cyclin. Modulation of the cyclin gene is used to increase or decrease the growth rate, provide faster germination, reduce time to flowering, increase the number of flowers, seeds or fruits per plant, increase root development, reduce height and to delay flowering in a range of plants, e.g. legumes, grasses, maize, oilseed rape, wheat, tomato, rice, barley, sunflower,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Regulating growth and structure of plants by modulating protein that controls cell division - specifically a D-type cyclin, and related chimeric genes and transformed cells and plants, used to alter growth rate, flowering, seed production etc.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 1846 BP; 448 A; 425 C; 514 G; 458 T; 1 other;
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 ATCATTACAAGTGATAGCCAGCACAACCAAAGGTATTGACTTTTTGGAGTTTAGACCTTC
                                                                                                                                                                                                                                                                          TGTGGCTTGTTATCATTGGCAGCCAAAATTGAAGAAACTGAAGTTCCAATGTTGATAGA 440
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GATGGTGGAGAAGGAGAAGCAGCATTTGCCAAGTGATGATTACATCAAGAGACT-----
                                     atactttcttcataaattgagtga---tcatggtgcaccctccttgcttgcacgctctcg
                                                                       ATATTTCCTGAGAAAGATGAGTAAATGTGATCAAGAACCATCCAACACATTGATATCTAG
                                                                                                           tttgcaggtagcggaggcaaagtttgtttttgagggaaggaccataaaaaggatggagct
                                                                                                                                                                                                                   TCTTCAGGTTGGAGATCCTCAGTTTGTGTTTGAGGCTAAATCAGTCCAAAGAATGGAGCT
                                                                                                                                                                                                                                                       agtggcttgcttgtctttggcttcgaaaatcgaagagacttttgtgccactccccttgga
                                                                                                                                                                                                                                                                                                                             tagattcctctccacgtatgagttccctgaaggcagagcttggatgactcagctcttggc
                                                                                                                                                                                                                                                                                                                                                                   TCGATTCTTATCGGTTCATGATTTGCCTAGTGGCAAAGGTTGGATATTGCAGTTGTTGGC
                                                                                                                                                                                                                                                                                                                                                                                                    ggtcattgagcattacaatttcgcaccgttgactgccgttttgtctgtgaactacctcga
                                                                                                                                                                                                                                                                                                                                                                                                                                       GGCTTGTGAAGTACACCAGTTTGGACCATTGTGTTTTTGCTTAGCAATGAACTACTTGGA 320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           acggcatggggacctggatttggccgccgtcaggaaggacgccatcgattggatttggaa
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Pred. No. 7.9e-45;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 19;
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                               The present sequence is that of an isoform of the maize ZmCycD gene that encodes cyclin D (CycD, see AAX79321), a protein necessary C C for progression from G1 into S phase. The encoded protein binds to CDK4, and the active CycD-CDK4 hyperphosphorylates retinoblastoma associated protein, releasing the E2F transcription factor which activates DNA synthesis. The invention provides maize CycD colynucleotides (see AAX94581-84) and polypeptides (see AAX99321-24) that are involved in cell cycle regulation. Also provided are recombinant expression cassettes (including ZmCycD in sense or antisense orientation), host cells, transgenic plants (especially corn, sorghum, sunflower, safflower, wheat, rice, alfalfa or oilseed Brassica) and antibody compositions. A claimed method of modulating the level of CycD protein in a cell comprises transforming the cell with a recombinant expression cassette comprising a CycD polynucleotide linked to a promoter, and growing the cell with a recombinant expression of the CycD protein in the cell. The CycD protein is present in an amount sufficient to alter cell drysion, increase the number of cell swifting increase conference alter cell arouth.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Novel polynucleotides encoding maize cyclin D isoforms 1, 2 and 3, related proteins and antisense RNA useful for control of cell cycle % \left( 1\right) =\left\{ 1\right\} =\left\{ 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2000-283589/24.
P-PSDB; AAY79321.
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dividing, improve transformation
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AAZ94583;
                                                 AAZ94583 standard;
                                                                                                                                                                                                                                                                                                           1024
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 increase the growth rate, increase crop yield, alter plant height or size, enhance or inhibit organ (seed, root, shoot, ear,
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                                                                                                                                                                                                                                                   CAACTCTTC 749
                                                                                                                                                                                                                                                                                                        cgagattgctgccagtgttgcacttgctgctatcggcgaatgcaggagttctgtaattga
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Cyclo protein in the cell. The Cyc protein is present in an amount sufficient to alter cell division, increase the number of cells sufficient to alter cell division, increase the number of cells dividing, improve transformation frequencies, alter cell growth, increase the growth rate, increase crop yield, alter plant height or size, enhance or inhibit organ (seed, root, shoot, ear, tassel, stalk, pollen, stamen) growth, produce organ ablation, produce parthenocarpic fruits, produce male sterile plants, produce embryogenic response, increase callus induction, provide positive selection, increase plant regeneration, alter the time that cells are arrested in Gl or GO phase or in a particular cell cycle, improve response to environmental stress including cycle, improve response to environmental stress including the increase the number of seeds per pod or ear, alter the lag time in card divisions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    activates DNA synthesis. The invention provides maize CycD polynucleotides (see AA794581-84) and polypeptides (see AA79321-24) that are involved in cell cycle regulation. Also provided are recombinant expression cassettes (including zmCycD in sense or antisense orientation), host cells, transgenic plants (especially corn, sorghum, sunflower, safflower, wheat, rice, alfalfa or oilseed Brassica) and antibody compositions. A claimed method of modulating the level of CycD protein in a cell comprises transforming the cell with a recombinant expression cassette comprising a CycD polynucleotide linked to a promoter, and growing the cell for a time sufficient to induce expression of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             gene that encodes cyclin D (CycD, see AAY79323), a protein necessary for progression from G1 into S phase. The encoded protein binds to CDK4, and the active CycD-CDK4 hyperphosphorylates retinoblastoma associated protein, releasing the E2F transcription factor which
                                     seed development, provide hormone independent cell growth, or increase the growth rate of cells in bioreactors. The level of CycD protein in the cells is transiently modulated by introducing CycD RNA or CycD polypeptides. CycD polynucleotides can be used to identify CycD interacting proteins. All claimed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present sequence is that of an isoform of the maize ZmCycD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 1; Page 122-124; 134pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Novel polynucleotides encoding related proteins and antisense
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P-PSDB; AAY79323.
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Query Match Best Local Similarity

16.9%;

Score 156.8; DB 2 Pred. No. 1.5e-34;

21;

Length 1173;

Sequence 1173 BP; 200 A; 366 C; 416 G;

191 T; 0 other;

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RESULT
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                                                                                                                                                             Zea mays.
                                                                                                                                                                                      Cyclin delta-2; corn; maize; transgenic plant; herbicide;
                                                                                                                                                                                                                                                                                                              AAZ19961 standard; cDNA; 1932 BP
23-MAR-1998;
                            19-MAR-1999;
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 98US-0078948
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                                                                                                                    Location/Qualifiers 275..1441
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plant breeding; s
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Query Match Best Local

Local Similarity

15.2%; 54.0%;

Score 140.6; DB 2 Pred. No. 7.3e-30;

DB 20;

Length

1932;

ω

Sequence 1932 BP;

409 A; 548 C; 633 G; 337

T; 5 other;

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This nucleotide sequence represents a portion of the cDNA insert conclose ceb5.pk0049.h5 encoding a portion (see AAV31897) of a corn cyclin delta-2 pk01ypeptide. The clone was isolated from a corn cc embryo (20 days after pollination) cDNA library. The invention cc relates to isolated nucleic acid fragments (see AAZ19953-66) encoding cc cyclin A, cyclin delta-1, cyclin delta-2 and cyclin delta-3 cc polypeptides (see AAV31889-902). It also relates to the construction cc of chimeric genes encoding all or a portion of a cyclin, in sense cc antisense orientation, where expression of the chimeric gene cc results in altered levels of the cyclin protein in a transformed cc of cell division in those cells. The nucleic acid fragments may be culture growth. The availability of nucleic acid sequences encoding cl large protein of cyclins should facilitate studies of cell cycle culture, increase the efficiency of gene transfer and help provide contents that may be effectioney of gene transfer and help provide contents that may be inseful as horbiciaes
                                                                                                                                                                                                                                                                                                                                                                                                                                                              New isolated plant cyclin genes, used to herbicides and for developing plant breed \ensuremath{\mathsf{herbicides}}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cahoon RE,
                                    enzymes that may be useful as herbicides.
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Matches 664 348 604 288 547 228 487 168 427 108 ATTGTGTTTTTGCTTAGCAATGAACTACTTGGATCGATTCTTATCGGTTCATGATTTGCC GGGTTTTTCTCAATCGGAGAGTGAGGAGATTATCATGGAGATGGTGGAGAAGGAGAAGCA 167 TAGTGGCAAAGGTTGGATATTGCAGTTGTTGGCTGTGGCTTGTTTATCATTGGCAGCCAA tctcactgcctacttggcagtgaactacctcgatcgcttcctctcgctgtctgaggtgcc TGGAAGAAGAGATGCCCTCAATTGGATTTGGAAGGCTTGTGAAGTACACCAGTTTTGGACC ccacatgccggggccgtgctacggcgacaggctgcggcggcggcggcggctgtctctgcgt 546 GCATTTGCCAAGTGATGATTACATCAAGAGACTTAGAAGTGGAGATTTGGATTTGAATGT ggacttgttcccgccgcagtcggaggaatgcgtggccggtctggtggagcgggaacggga 486 ---ccgccgggaggccgtcgactggatttggaaggcttacacgcaccacggttccgccc 356; Conservative 0; Mismatches 294; Indels 9; Gaps 227 407 603 723 663 347 287

δÃ Db 20 В Qy 멍 δÃ DЬ QY DЬ Qy

Дb Qy Дb

844 525 784 465 724 408

GAGATTGAGAGCAATAACTCCATGCTCATACATAAGATATTTCCTGAGAAAGATGAGTAA

gaggatgcatgccgtgacgccgttctcctacgtggattacttcctgaacaagctcaacaa

TGTGTTTTGAGGCTAAATCAGTCCAAAGAATGGAGCTTTTGGTGTTTGAACAATTGAAATTG gatggaggaaaccgccgtcccgcagtgcctggaccttcaggaggtcggagacgcgcggta AATTGAAGAAACTGAAGTTCCAATGTTGATAGATCTTC---AGGTTGGAGATCCTCAGTT

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cgtgttcgaggcgaagacggtccagaggatggagctcctggttctaacaaccctcaactg

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RESULT 1
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Best Local S
Matches 309
                                                                                                                                                                                rate, provide faster germination, reduce time to flowering, increase the number of flowers, seeds or fruits per plant, increase root development, reduce height and to delay flowering in a range of plants, e.g. legumes, grasses, maize, oilseed rape, wheat, tomato, rice, barley, sunflower,
                                                                                                                                                                                                                                        This sequence represents the CYCD3;1 cDNA from Nicotiana tabacum which encodes a D-type cyclin. The sequence can be used to alter the growth characteristics or architecture of plants by altering the (functional) level in the plant cells of a cell-division controlling protein that can bind to, or phosphorylate, an Rb-like protein, such as a D-type cyclin. Modulation of the cyclin gene is used to increase or decrease the growth rate provide feater consideration and the cyclin gene is used.
                                                                                                                                                                                                                                                                                                                                                                                                Regulating growth and structure of plants by modulating protein th controls cell division - specifically a D-type cyclin, and related chimeric genes and transformed cells and plants, used to alter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 1998-532012/45.
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                                                                                                                                      Sequence 1679 BP; 537 A; 281 C;
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                           GATGCCCTCAATTGGATTTGGAAGGCTTGTGAAGTACACCAGTTTGGACCATTGTGTTTT 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              development;
gattctgtggaatggattttaaaaagtgaatggttattatggtttctctctgctttgactgcc
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                                                                           Similarity
                                                                                                                                                                   chrysanthemum, rose,
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                                                                                    CAMBRIDGE TECH SERVICES LTD.
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                                                                                                                                    98WO-EP01701
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Regulating growth and structure of plants by modulating protein that controls cell division - specifically a D-type cyclin, and related $\,$

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RRESULT 1
AAV33BAY
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AC AAV3
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                 01-OCT-1998
                                                                                                                                                                                       H.tuberosus
                                                                                                                                                                                                                       25-JAN-1999
                                                                                                                                                                                                                                                                                           AAV33887 standard; cDNA to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 1414 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       chimeric genes and transformed cells and plants, used growth rate, flowering, seed production etc.
                                                                                   Helianthus tuberosus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    carnation, chrysanthemum, rose, tulip, etc.
                                                                                                                                                                                                                                                                                                                                                                             677
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nes 218; Conserv
                                                                                                                                                                                                                                                                                                                            12
                                                                                                                   development;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TGTGTTTGAGGCTAAATCAGTCCAAAGAATGGAGCTTTTTGGTGTTGAACAAATTGAAATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CAAAATTGAAGAAACTGAAGTTCCAATGTTGATAGATCTTCAGGTTGGAGATCCTCAGTT
                                                                                                                                                                                                                                                                                                                                                                          aactgatcatg
                                                                                                                                                                                                                                                                                                                                                                                                           ATGTGATCAAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cttgtttgaggctaaaaacatacaaaaaatggagcttttggtgatgtcaactttgaaatg
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TGTTGGAAGAAGAAGATGCCCTCAATTGGAATTTGGAAGGCTTGTGAAGTACACCAGTTTGG 284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              tcaagaagataaaccttggatgattcaacttgttgctgttagttgtctctctttagctgc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              {\tt ACCATTGTGTTTTTGCTTAGCAATGAACTACTTGGATCGATTCTTATCGGTTCATGATTT}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                tgctgctcgtaaagaggctgtagattggatccttaaggtcaaaagttgttatggattcac
                                                                                                                                                  cyclin;
                                                                                                                                   retinoblastoma;
                                                                                                                                                                                    CYCD1;1 gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     represents the
                                                                                                                                                    growth; plant; cell-division control;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        75pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    449 A; 276 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  13.6%;
                                                                                                                                   germination;
                                                                                                                                                                                                                                                                                           mRNA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 126.2;
Pred. No. 7.7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches 153;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    248 G; 441 T; 0 other;
                                                                                                                                 flowering; seed; fruit;
                                                                                                                                                                                                                                                                                           ВP
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                                                                                                                                                    phosphorylation;
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ccgtttagctttatcggcttcttttcgcacaaaatcgatccatctggaatgtatacgggt

TTGGAGTTTAGACCTTCTGAAGCTGCTGCTGCTGGCACTTTCTGTTTCTGGAGAATTG ttc---cttatctcaagggcaacacaaattatcctctcaaatattcaagaagctagttta

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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This sequence represents the CYCD1;1 cDNA from Helianthus tuberosus which encodes a D-type cyclin. The sequence can be used to alter the growth characteristics or architecture of plants by altering the (functional) level in the plant cells of a cell-division controlling protein that can bind to, or phosphorylate, an Rb-like protein, such as a D-type cyclin. Modulation of the cyclin gene is used to increase or decrease the growth rate, provide faster germination, reduce time to flowering, increase the number of flowers, seeds or fruits per plant, increase root development, reduce height and to delay flowering in a range of plants, e.g. legumes, grasses, maize, oilseed rape, wheat, tomato, rice, barley, sunflower,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Regulating growth and structure of plants by modulating protein controls cell division - specifically a p-type cyclin, and relat chimeric genes and transformed cells and plants, used to alter growth rate, flowering, seed production etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 1788
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 14; p56-57; 75pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               carnation,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 1998-532012/45
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 544
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                                                                                                                          GTTCCAATGTTGAGATCTTCAGGTTGGAGATCCTCAGTTTGTGTTTTGAGGCTAAATCA
                                                                                                                                                                                                                                                               GCAATGAACTACTTGGATCGATTCTTATCGGTTCATGATTTGCCTAGTGGCAAAGGTTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GAGAGTGAGGAGATTATCATGGAGATGGTGGAGAAGGAGGAGCAGCATTTGCCAAGTGAT 183
CCATGCTCATACATAAGATATTTCCTGAGAAAGATGAGTAAATGTGATCAAGAACCATCC
                                  atccgaagaatggagtttcttgtgcttagtgtttttggattggagactaagatccgttaca
                                                    GTCCAAAGAATGGAGCTTTTGGTGTTGAACAAATTGAAATGGAGATTGAGAGCAATAACT
                                                                                                      attccttctattcttgatctccaggttgaaggtgcaaaatatatttcgagccgaaaaca
                                                                                                                                                                           cccttgcaactcttatctgtagcatgcttgtctttagctgctaaaatggaggaaaccctt
                                                                                                                                                                                                                                                                                                                                                  CTCAATTGGAATTTGGAAGGCTTGTGAAGTACACCAGTTTGGACCATTGTGTTTTTGCTTA 303
                                                                                                                                                                                                                                                                                                                                                                                   gattacgtcgagcgatttcaatcgcaagttctcgat---gcttctgctagagaagaatcg
                                                                                                                                                                                                                                                                                                                                                                                                                     GATTACATCAAGAGACTTAGAAGTGGAGATTTGGATTTGAATGTTGGAAGAAGAGATGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATATTGCAGTTGTTGGCTGTGGCTTGTTTATCATTGGCAGCCAAAATTGAAGAAACTGAA
                                                                                                                                                                                                                                           tccgttaactatctggatcgtttcatctattgccgtggcttcccggtggcaaatgggtgg
                                                                                                                                                                                                                                                                                                              gttgcctggatccttaaggtgcaacggttttacggatttcagccgttgacggcgtacctc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           325;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      97EP-0302096
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             511 A; 386 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          13.3%; 52.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               rose, tulip,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SERVICES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 123.2; DI
Pred. No. 6e-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             387 G;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              504 T; 0 other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          293;
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                                                                      543
                                                                                                                                          483
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AAV33886
                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                                                                                                                  This sequence represents the CYCD3;2 cDNA from Nicotiana tabacum which encodes a D-type cyclin. The sequence can be used to alter the growth characteristics or architecture of plants by altering the (functional) level in the plant cells of a cell-division controlling protein that can bind to, or phosphorylate, an Rb-like protein, such as a D-type cyclin. Modulation of the cyclin gene is used to increase or decrease the growth rate, provide faster germination, reduce time to flowering, increase the number of flowers, seeds or fruits per plant, increase root development, reduce height and to delay flowering in a range of plants, e.g. legumes, grasses, maize, oilseed rape, wheat, tomato, rice, barley, sunflower, carnation chryganthemum race, tilin other, and the control of the cyclin of the c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Regulating growth and structure of plants by modulating protein controls cell division - specifically a D-type cyclin, and relat chimeric genes and transformed cells and plants, used to alter growth rate, flowering, seed production etc.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   D-type cyclin; growth; plant; cell-division control; phosphorylation; CDC; Rb; retinoblastoma; germination; flowering; seed; fruit;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAV33886 standard; cDNA to mRNA; 1431
                                                                                                                                                                                                                                                                                                                                          Sequence 1431 BP;
                                                                                                                                                                                                                                                                                                                                                                                        carnation,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 14; p55-56; 75pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (UYCA-) UNIV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        26-MAR-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   root
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         N. tabacum CYCD3;2 gene
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAV33886;
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  CTTATCGGTTCATGATTTGCCTAGTGGCAAAGGTTGGATATTGCAGTTGTTGGCTGTGGC
                                                                                                                                                           TGGAGATTTGGAATGTTGGAAGAGAGAGAGGCCCCCAATTGGATTTGGAAGGCCTTG 266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1998-532012/45
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                                                                        TGAAGTACACCAGTTTGGACCATTGTGTTTTTGCTTAGCAATGAACTACTTGGATCGATT 326
                                                                                                                                    tggagatgggtttttagtggaggttagaaaagaggcattggattggatgttgagagtcat 502
                                              tyctcactatggtttcactgctatgactgctgttttagctgtgaattattttgataggtt 562
                                                                                                                                                                                                                               212;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           97EP-0302096.
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                                                                                                                                                                                                                                                                                                                                          387 A; 267 C;
                                                                                                                                                                                                                                                 12.8%;
                                                                                                                                                                                                                                                                                                                                                                                    rose,
                                                                                                                                                                                                                               0;
                                                                                                                                                                                                                          Score 118.4;
Pred. No. 1.2e
0; Mismatches
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                                                                                                                                                                                                                                                 1.2e-23;
                                                                                                                                                                                                                                                                      DB 19;
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                                                                                                                                                                                                                            0;
                                                                                                                                                                                                                          Gaps
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16-APR-1999;
19-APR-1999;
                         14-MAY-1999;
18-MAY-1999;
19-MAY-1999;
20-MAY-1999;
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06-MAY-1999;
07-MAY-1999;
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30-APR-1999;
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23-APR-1999;
23-APR-1999;
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01-APR-1999;
06-APR-1999;
                                                                                                               14-MAY-1999
14-MAY-1999
                                                                                                                                                                                                                                                                      04-MAY-1999
05-MAY-1999
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                                                                                                                                                              14-MAY-1999
                                                                                                                                                                                11-MAY-1999
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25-MAR-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     09-MAR-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  25-FEB-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        metabolic pathway; promoter;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Arabidopsis thaliana DNA fragment SEQ ID
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      gctctccactcttaagtggaaaatgaatccagtgacaccactatctttcattgatcatat 802
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              agtggctgattcaagatttgtgttttgaggcaaagactattcagagaatggaactcttggt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ttgtctttctattgctgctaaagtggaagagacccaagtcccccttctcttagacctcca
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          tgtatctggactctgctttcagaaagataagccttggatgagtcaacttgctgctgtggc
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990S-0126785
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990S-0128714
990S-013077
990S-0130449
990S-0130910
990S-0131449
990S-0132407
990S-0132407
990S-0132466
990S-0132485
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990S-0132487
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990S-0134276
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99US-0123548
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signal transduction pathway;
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28-MAY-1999 01-JUN 1999; 03-JUN 1999; 04-JUN 1999; 07-JUN 1999; 10-JUN 1999; 11-JUN 1999; 11-	24-MAY-1999; 25-MAY-1999; 27-MAY-1999;
990S-0137222 990S-0137222 990S-0137222 990S-0137222 990S-0137222 990S-0138044 990S-0138847 990S-0139453 990S-0139453 990S-0139456 990S-0139456 990S-0139460 990S-0139460 990S-0139460 990S-0139462 990S-0139763 990S-0139763 990S-0140695 990S-0144086 990S-0144085 990S-0144085 990S-0144086 990S-0145086 990S-0145913 990S-0145913 990S-0145913	99US-0135629. 99US-0136021. 99US-0136392.
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990S-0147192. 990S-0147260. 990S-0147260. 990S-0147416. 990S-0147935. 990S-0148311. 990S-0148341. 990S-0149368. 990S-0149368. 990S-0149368. 990S-0149929. 990S-0151080. 990S-0151303. 990S-0155659. 990S-0157753. 990S-0157753. 990S-0158029. 990S-0158029. 990S-0159331. 990S-0159331. 990S-0159331. 990S-0159331. 990S-0159331. 990S-0159331. 990S-0159638. 990S-0159638. 990S-0160767. 990S-0160767. 990S-0160767. 990S-0160981. 990S-0161405. 990S-0161405. 990S-0161405. 990S-0161405. 990S-01613636. 990S-01613636.	

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Best Local Sim
Matches 203;
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42423
25-FEB-1999

05-MAR-1999

09-MAR-1999

23-MAR-1999

25-MAR-1999

20-MAR-1999

01-APR-1999

06-APR-1999

06-APR-1999

16-APR-1999

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28-OCT-1999;
29-OCT-1999;
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                                                                                                                                                                                                                                                              Arabidopsis thaliana
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                                                                                                                                                                                                                                                                                                                                                                                                                                           GAACAAATTGAAATTGAGAGTTGAGAGCAATAACTCCATGCTCATACAT 557
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATCGGTTCATGATTTGCCTAGTGGCAAAGGTTGGATATTGCAGTTGTTGGCTTGGCTTG
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99US-0161993.
99US-0162142.
990S-0121825.
990S-012548.
990S-0125548.
990S-0125788.
990S-0126764.
990S-0127462.
990S-0128734.
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990S-0130840.
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990S-0131448.
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Pred. No. 5.7e-23;
0; Mismatches 145;
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07-MAY-1999
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11-JUN-1999
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06-MAY-1999;
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Search completed: January 21, 2002, 00:21:58 Job time: 2927 sec

13-OCT-1999; 13-OCT-1999; 14-OCT-1999; 14-OCT-1999; 14-OCT-1999; 14-OCT-1999; 14-OCT-1999; 21-OCT-1999; 21-OCT-1999; 21-OCT-1999; 21-OCT-1999;

08-OCT-1999; 12-OCT-1999; 13-OCT-1999;

990S-0151066 990S-0151080 990S-0151303 990S-0151303 990S-0152363 990S-015376 990S-0154018 990S-0154018 990S-0155139 990S-0156458 990S-0156458 990S-0156458 990S-0157753 990S-0157753 990S-0157865 990S-0158232 990S-0159294 990S-0159293 990S-0159293 990S-0159294 990S-0159293 990S-0159331 990S-0159638 990S-0159638 990S-0159638 990S-0159638 990S-0159638 990S-0159638

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Result
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2: /cgn2_6/prodata/2/ina/5B_COMB.seq:*
3: /cgn2_6/prodata/2/ina/6A_COMB.seq:*
4: /cgn2_6/prodata/2/ina/6B_COMB.seq:*
5: /cgn2_6/prodata/2/ina/PCTUS_COMB.seq:*
6: /cgn2_6/prodata/2/ina/backfiles1.seq:*
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US-09-222-851-18
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US-09-222-851-18
US-08-32-6-691B-51
US-08-347-120-7
US-08-447-120-7
US-08-447-492-7
US-08-460-694-1
US-08-767-711B-1
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US-08-895-770-5
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US-08-895-770-8
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532	472 655	412 598	352 544	292 484	232 424	Query Mat Best Loca Matches	SULT 1 -09-092-770- Sequence 8, Patent No. 5 GENERAL INEG APPLICANT: APPLICANT: APPLICANT OF IN FILE REFERE CURRENT APPL UNMBER OF S SOFTWARE: p SEO ID NO 8 LENGTH: 12 TYPE: DNA ORGANISM: ORGANISM:		4444443337 33228 444449 44324 5432 5432
AGAGCAATAACTCCATGCTC	GAGGCTAAATC : wsngargarga	GAAGAAACTGAAGTTCCAATGTTG : :	GGCAAAG aaraa	TGTTTTTG : acnttyta	AGAAGAG : :: mgnwsna	Match ocal Simis 110;	1 12-770-8 12-770-8 10-00-8, Application U 10-00-8, Application U 10-00-8, Application U 10-00-9, Steven 10-00-8, Steven 10-00-8, Steven 10-00-8, Steven 10-00-8, Steven 10-00-8, Steven 10-00-8, Steven 10-00-8, Application U 10-00-8, Application U 10-00		332 332 332 332 334 344 344 344 344 344
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CATGCT	CAAA : : ytnm	TTCCAATGT	TATTGC : tgytnc	CAATO :	TCAATT	5. 32. ative	2 75 57 5		1311 1680 1680 1680 1680 1680 1680 11680 1692 1951 11225 1971 11225 1971 11225 1971 11225 1971 11225 1971 11225 1971 11225 1971 1971 1971 1971 1971 1971 1971 197
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ATACATAAGATATTTCCT 569	TGGAGCTTTTGGTGTTTGAACAAT ::	ATAGATCTTCAGGTTGGAGATC : : cargarttygcntaygtna	TGTTGGCTGTGGCTTGTTTATCATT 	ACTTGGATCGATTCTTATCGGTTCATG	TTTGGAAGGCTTGTGAAGTAC : : : tnytngargtntgygargtnt	Score 48; DB 2; Length Pred. No. 0.00019; 60; Mismatches 159; Inde	92770 19el Cyclin E Genes and 5/09/092,770 05	ALIGNMENTS	US-09-027-007-4 US-08-706-539-1 US-08-522-166-1 US-08-488-382A-1 US-08-488-312-1 US-08-480-912-1 US-08-480-912-1 US-08-485-859-1 US-08-895-707-1 5182210-9 US-08-866-650-2 US-09-221-287-2 US-09-221-287-2 US-09-245-041-18 US-09-245-041-18 US-09-245-041-16
	TGAAATGGAGATTG : :: tnaartgggarytn	AGTTTGTGTTT : ayggngcntgy	GGCAGCCAAAATT : : hgcnwsnaarytn	GATTTGCCTAGT : : aargayathaay	ACCAGTTTGGACCATTG : : ; : ayacnytncaymgngar	1215; ls 9; Ga	Proteins		Sequence 1, Sequence 1, Sequence 1, Sequence 1, Sequence 1, Sequence 1, Sequence 1, Sequence 1, Sequence 2, Sequence 2, Sequence 2, Sequence 2, Sequence 2, Sequence 2, Sequence 1, Sequence 1, Sequence 2, Sequence 1, Sequence 1, Sequence 1, Sequence 1,
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; SEQ ID NO 8
; LENGTH: 1215
; TYPE: DNA
; ORGANISM: Human
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LENGTH: 1212
TYPE: DNA
ORGANISM: Mouse
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                                                                                                                                                                                                                                                                                                                                          Sequence 18, Application US/09092770 Patent No. 5973119
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                                                                                                                                 CURRENT APPLICATION NUMBER: US/09/092,770 CURRENT FILING DATE: 1997-06-05 NUMBER OF SEQ ID NOS: 18
                                                                                                                                                                                                    APPLICANT: Coats, Steven R.
APPLICANT: Bass, Michael B.
APPLICANT: Robinson, Murray O.
TITLE OF INVENTION: No. 5973119el Cyclin E Genes
FILE REFERENCE: A-524
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09-092-770-18
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EARLIER FILING DATE: 198-06-05
NUMBER OF SEO ID NOS: 18
SOFTWARE: Patentin Ver. 2.0
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APPLICANT: Robinson, Murray O.
TITLE OF INVENTION: No. 6165753el Cyclin E
FILE REFERENCE: A-524
                                                                                                              SOFTWARE:
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CURRENT FILING DATE: 1998-12-30
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les 110; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; TYPE: DNA
; ORGANISM: Mouse
US-09-222-851-18
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EARLIER APPLICATION NUMBER: 09/092,770 EARLIER FILING DATE: 1998-06-05 NUMBER OF SEQ ID NOS: 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Coats, Steven R.
APPLICANT: Bass, Michael B.
APPLICANT: Robinson, Murray O.
TITLE OF INVENTION: No. 6165753el Cyclin E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION NUMBER: US/09/222,851
CURRENT FILING DATE: 1998-12-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: PatentIn Ver.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILE REFERENCE: A-524
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                                            595 gargarathtaygcnccnaarytncargarttygcntaygtnacngayggngcntgywsn 654
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nes 106; Conserv
GAGGCTAAATCAGTCCAAAGAATGGAGCTTTTGGTGTTGAACAAATTGAAATGGAGATTG 531
                                                                                           GAAGAAACTGAAGTTCCAATGTTGATAGATCTTCAGGTTGGAGATCCTCAGTTTGTGTTT 471
                                                                                                                                          gtnaayaaraayatgytncarytnathggnathacnwsnytnttyathgcnwsnaarytn
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                                                                                                                                                                                                                                                                                                                                                                                                                              4.7%; Score 43.6; DB 4; Length 1212; 31.4%; Pred. No. 0.0034; ative 60; Mismatches 163; Indels 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4.7%;
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Pred. No. 0.0034;
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US-08-232-463-14
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: EP 91
FILING DATE: 26-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,76
                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
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APPLICANT:
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/232,463
IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)836-9300
TELEFAX: (703)683-4109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                               712 tgyccngtnacngtnathwsntggytnaayytnttyyt 749
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                                                                                               63 CATGATTGTTGACGAAACTCCGATTGAAATTTCGATTCCTCAGATGGGTTTTTCTCAATC 122
                                                                                                                                                                                                 Local Similarity nes 19; Conserv
                                                                                                                                                                                                                                                                                                                                                  LENGTH: 7218 base pairs TYPE: nucleic acid STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY:
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                                                                INFORMATION:
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VENTION: RECOMBINANT FOWLPOX VIRUS
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linear
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;; Pred. No. 0.055;
166; Mismatches 130;
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                                                                                                                                                                                                 Indels
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US-08-306-691B-51
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Best Local 9
                                                                                                                                                                            Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OPERATING SYSTEM: MS-DOS
SOFTWARE: WORDERfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08,
FILING DATE: September 15
                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS
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TELEPHONE: (215) 568-8383
TELEFAX: (215) 568-5549
                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
NAME: Monaco, Daniel A.
REGISTRATION NUMBER: 30,
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1099 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRATCGCAAGCTCCCTCGACCTGCAGCCA 1040
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361 TGGATATTGCAGTTGTTGGCTGTGGCTTGTTTATCATTGGCAGCCAAAATTGAAGAAACT 420
                                                                  301
                                                                                                     322
                                                                                                                                         241 GCCCTCAATTGGATTTGGAAGGCTTGTGAAGTACACCAGTTTGGACCATTGTTTTTTGC 300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             183 TGATTACATCAAGAGACTTAGAAGTGGAGATTTGGATTTGAATGTTGGAAGAAGAGATGC
                                   382 CTGGCCATGAACTACCTGGACCGCTTCCTGTCGCTGGAGCCCGTG
                                                                                                                                                                                           Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY: U
ZIP: 19102
                                                                                                                                                                                                                                                                                                   STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: Seidel, Gonda, Lavorgna & Monaco, P.C. STREET: Two Penn Center, Suite 1800
                                                                                                                                                                                                                                                                                    TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                        LENGTH: 1325 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CCTCAATTGGATTTGGAAGGCTTGTGAAGTACACCAGTTTGGACCATTGTGTTTTTGCTT 302
                                                                TTAGCAATGAACTACTTGGATCGATTCTTATCGGTTCATGATTTGCCTAGTGGCAAAGGT 360
                                                                                                     GTCGCCACCTGGATGCTGGAGGTCTGCGAGGAACAGAAGTGCGAGGAGGAGGTCTTCCCG 381
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                                                                                                                                                                          165;
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                                                                                                                                                                                                                                                                                                                 nucleic acid
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                                                                                                                                                                            Conservative
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OLIGONUCLEOTIDES TARGETING COOPERATING ONCOGENES
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                                                                                                                                                                                         Score 35.8;
Pred. No. 0.
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RESULT 7
US-07-947-120-7
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; LOCATION:
US-07-947-120-7
                20
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                                                                                                                   Matches 165;
                                                                                                                                Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/07/947
FILING DATE: 19920917
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Lauder, Leona L.
REGISTRATION NUMBER: 30,863
REFERENCE/DOCKET NUMBER: 91-2
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                               TELEFAX: 415-543-4219
INFORMATION FOR SEQ ID NO: 7
SEQUENCE CHARACTERISTICS:
LENGTH: 4221 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT:
                                                                                                                                                                                                                                                                MOLECULE TYPE:
HYPOTHETICAL:
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301 TTAGCAATGAACTACTTGGATCGATTCTTATCGGTTCATGATTTGCCTAGTGGCAAAGGT 360
                                                  319 GTCGCCACCTGGATGCTGGAGGTCTGCGAGGAACAGAGTGCGAGGAGGAGGTCTTCCCG 378
                                                                                 241 GCCCTCAATTGGATTTGGAAGGCTTGTGAAGTACACCAGTTTGGACCATTGTGTTTTTGC 300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: PatentIn Release #1.0, Version #1.25
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                                                                                                                                                                                                                                                                                                               STRANDEDNESS:
                                                                                                                                                                                                                                                                                                   FOPOLOGY:
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Steuart Street Towe
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VENTION: BC1-1 Locus Nucleic Acid Probes
                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
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142..1026
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48.7%;
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                                                                                                                     0; Mismatches
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                                                                                                                                Score 35.8;
Pred. No. 1;
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                                                                                                                                                     DB 1;
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                                                                                                                                                     Length 4221;
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RESULT 8
US-08-472-893A-7
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US-08-472-893A-7
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                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: 415-543-4219
INFORMATION FOR SEQ ID NO: ::
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE: 435
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION UNBER: US 07/947,120
APPLICATION 17-SEP-1992
TOTAL TO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/472,89: FILING DATE: 07-JUN-1995
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MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: 17-SEP-1992
ATTORNEY/AGENT INFORMATION:
NAME: Lauder, Leona L.
REGISTRATION NUMBER: 30,
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-777-9257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
                                                                                                           FEATURE:
                                                                                                                                                                            TOPOLOGY: 1: MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                421 GAAGTTCCAATGTTGATAGATCTTCAGGTTGGAGATCCTCAGTTTGTGTTTTGAGGCTAAA 480
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                                                                                                                                              HYPOTHETICAL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     361 TGGATATTGCAGTTGTTGGCTGTGGCTTGTTTATCATTGGCAGCCAAAATTGAAGAAACT 420
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STREET: Plaza
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ZIP: 94105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CITY: San Francisco
STATE: CA
                              NAME/KEY:
LOCATION:
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                                                                                                                                                                                                                                                                                            nucleic acid
                                                                                                                                                                                                                                                                                                                                  4221 base pairs
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                                      142..1026
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Query Match
Best Local Similarity
Matches 165; Conserv

Conservative

0;

3.9%; 48.7%;

Score 35.8; Pred. No. 1; Mismatches

DB 1;

Length 4221; Indels

162;

12;

Gaps

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US-08-947-492-7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
APPLICANT: Meeker
                                                                                                                                                                                                      TELEFAX: 415-543-4219 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Meeker, Timothy C.
TITLE OF INVENTION: BC1-1 Locus Nucleic Acid Probes and
TITLE OF INVENTION: Assay Methods
                                                                                                                                             SEQUENCE CHARACTERISTICS:
LENGTH: 4221 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER: 91
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-777-9257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: PatentIn Release #1.0, Version #1. CURRENT APPLICATION DATA:
                                                                                          TOPOLOGY: 1
MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                      FEATURE:
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                                                                        HYPOTHETICAL:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              547
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               NAME/KEY:
LOCATION:
                                                                                                                                                                                                                                                                                                NAME: Lauder, Leona L. REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: Leona L. Lauder
STREET: Steuart Street Tower,
                                                                                                                           STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE:
                                                                                                                                                                                                                                                                                                                                                          FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER:
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142..1026
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US-08-460-694-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 1, Application US/08460694 Patent No. 5858655
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
                                                                                                                                       TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                         TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION: NAME: McConathy, Evelyn
                                                                                                                                                                                                                                                                                                                                      SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS: ADDRESSEE: STERNE, K
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                                               FEATURE:
                                                            TOPOLOGY: 1
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                                                                                                               TYPE: r
                                                                                                                                                                                                                        NAME: McConathy, Evelyn H. REGISTRATION NUMBER: 35,279 REFERENCE/DOCKET NUMBER: 06
                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                           STRANDEDNESS:
                                                                                                                                                                                                                                                                                        CLASSIFICATION:
                                                                                                                                                                                                                                                                                                       FILING DATE:
                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY:
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               LOCATION:
                            NAME/KEY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TCAGTCCAAAGAATGGAGCTTTTGGTGTTGAACAAATTGAAATGGAGATTGAGAGCAATA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -- CATCCCCCTGACGGCCGAGAAGCTGTGCATCTACACCGACAACTCCATCCGGCCCGAG
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                                                                                                                         4244 base pairs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       USA
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               CDS
148..1035
                                                                            ss: single
linear
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Pred. No. 1;
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                                                                                                                                                                                                                                                                                                                                                        Version
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Suite
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Patent No. 6107541
-08-460-744-1
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Best Local Similarity
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                                                                                                                                         TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
LENGTH: 4244 base pairs
                                                                                                                                                                                                REFERENCE/DOCKET NUMBER: 06
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEPAX: 202-371-2540
                                                                                                                                                                                                                                                                CLASSIFICATION: 4...
CLASSIFICATION: 4...
ATTORNEY/ACENT INFORMATION:
NAME: McConathy, Evelyn H.
NAME: McConathy, 5.76
                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION UNMBER: US/08/460,744 FILING DATE: 02-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Arnold, TITLE OF INVENTION:
                                                      FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS
                                                                         MOLECULE TYPE:
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                                                                                                                            TYPE:
                                                                                            TOPOLOGY: 11
                                                                                                                                                                                                                                                                                                                   CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                     NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY:
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                    LOCATION:
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Pred. No. 1;
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Best Local Similarity
                                                                                                                                          TELEFAX: (202) 371-25
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                           CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                       ZIP: 20005
COMPUTER READABLE FORM:
                                FEATURE:
                                                MOLECULE TYPE:
                                                                                                                            SEQUENCE CHARACTERISTICS:
                                                                                                                                                                            TELEPHONE: (202) 371-2600
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                                                           STRANDEDNESS: C
NAME/KEY:
                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER:
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Prad1 Cyclin and Its cDNA
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Pred. No. 1;
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RESULT 13
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US-08-770-761A-4
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Best Local Similarity
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                                                                                                                              INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Rao, Ramachandra N.
TITLE OF INVENTION: FUSION PROTEINS COMPRISING CELL CYCLE
TITLE OF INVENTION: REGULATORY PROTEINS
NUMBER OF SEQUENCES: 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Kovacevic, Ste
APPLICANT: Otto, Keith A.
APPLICANT: Rao, Ramachand
                 MOLECULE TYPE:
                                                                 SEQUENCE CHARACTERISTICS:
LENGTH: 4453 base pairs
TYPE: nucleic acid
                                                                                                                                                                  TELECOMMUNICATION INFORMATION: TELEPHONE: 317-376-0756
                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
NAME: Gaylo, Paul J.
REGISTRATION NUMBER: 36,808
                                                                                                                                                                                                                                                                                                                                  SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
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                                   TOPOLOGY:
                                             STRANDEDNESS: single
                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                  CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                           OPERATING SYSTEM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CITY: Indianapolis
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                                                                                                                                                  TELEFAX:
                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US/08/770,761A
                                                                                                                                                                                                                                                                                                                                                                                                               MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GAGCTGCTGCAAATGGAGCTGCTCCTGGTGAACAAGCTCAAGTGGAACCTGGCCGCAATG 612
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           --CATCCCCCTGACGGCCGAGAAGCTGTGCATCTACACCGACAACTCCATCCGGCCCGAG 552
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Lilly Corporate Center/Patent Division
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                                                                                                                                                  317-277-1917
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                                                                                                                                                                                                                                                                                                                                                                         E: Floppy disk
IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eli Lilly and Company
                                                                                                                                                                                                                                                                                      19-DEC-1996
N: 530
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48.78;
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Pred. No. 1
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US-08-770-761A-6
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Best Local Similarity
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                                                                                                                          TELEPHONE: 317-376-0756
TELEFAX: 317-277-1917
INFORMATION FOR SEQ ID NO: (
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             TOPOLOGY: 1
MOLECULE TYPE:
                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
NAME: Gaylo, Paul J.
REGISTRATION NUMBER: 36,808
                                                                                                                                                                                                                                                                                                              SOFTWARE: Patentin Rel
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Rao, Ramachandra N.
TITLE OF INVENTION: FUSION PROTEINS COMPRISING CELL CYCLE
TITLE OF INVENTION: REGULATORY PROTEINS
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APPLICANT:
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                                                                                                         SEQUENCE CHARACTERISTICS:
                                                                                                                                                                             TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                          FILING DATE: 19
CLASSIFICATION:
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                                                STRANDEDNESS:
                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER:
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                                                                                   LENGTH:
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                                                                  nucleic acid
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                                                                                     4540 base pairs
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Lilly Corporate Center/Patent Division
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                                   linear
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N: 530
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Pred. No. 1;
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US-08-770-761A-1
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; MOLECULE TYPE: US-08-770-761A-1
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Best Local
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                                                                                                                                              TELEFAX: 317-277-1917
INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Kovacevic, Steven
APPLICANT: Otto, Keith A.
APPLICANT: Rao, Ramachandra N.
TITLE OF INVENTION: FUSION PROTEINS COMPRISING CELL CYCLE
TITLE OF INVENTION: REGULATORY PROTEINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2703
                                                                                                      SEQUENCE CHARACTERISTICS:
LENGTH: 4621 base pairs
                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
NAME: Gaylo, Paul J.
REGISTRATION UNMBER: 36,808
REFERENCE/DOCKET NUMBER: X-:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: DOS PC-DOS/MG-DOS
OPERATING SYSTEM: PC-DOS/MG-DOS
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CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: PatentIn Release #1.0, Version CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    241 GCCCTCAATTGGAATTTGGAAGGCTTGTGAAGTACACCAGTTTTGGACCATTGTGTTTTTGC 300
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                                                                                                                                                                                                                                                                                                                    FILING DATE: 19 CLASSIFICATION:
                                        STRANDEDNESS:
TOPOLOGY: li
                                                                                    TYPE: nucleic acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CITY: Indianapolis
                                                                                                                                                                       TELEPHONE: 317-376-0756
TELEFAX: 317-277-1917
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                                                                                                    ENGTH:
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Similarity 48.7%;
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ON: 530
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                                                                                                                                                                                                                                   x-10136
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                                                                                                                                                                                                                                            2595
                                                                                                                                                                                                                                                                                                                                                                                                    2484 GTCGCCACCTGGATGCTGGAGGTCTGCGAGGAACAGAAGTGCGAGGAGGAGGTCTTCCCG 2543
                                                                                                                                                                                                                                                                                                                         2544 CTGGCCATGAACTACCTGGACCGCTTCCTGTCGCTGGAGCCCGTG------AAAAAG 2594
                                                                                                                                                          2654 --CATCCCCCTGACGCCGAGAAGCTGTGCATCTACACCGACAACTCCATCCGGCCCGAG
                      541 ACTCCATGCTCATACATAAGATATTTCCTGAGAAAGATG 579
                                                                                                                                                                                                                                                                                                                                                                                                                               241 GCCCTCAATTGGATTTGGAAGCTTGTGAAGTACACCAGTTTGGAACCATTGTGTTTTTGC 300
                                                                                                481 TCAGTCCAAAGAATGGAGCTTTTGGTGTTGAACAAATTGAAATTGGAGATTGAGAGCAATA 540
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                                                                                                                                                                                                                                                                                                                                              TTAGCAATGAACTACTTGGATCGATTCTTATCGGTTCATGATTTGCCTAGTGGCAAAGGT 360
                                                                           GAGCTGCTGCAAATGGAGCTGCTCCTGGTGAACAAGCTCAAGTGGAACCTGGCCGCAATG
                                                                                                                                                                                                                                                                               TGGATATTGCAGTTGTTGGCTGTGGCTTGTTTATCATTGGCAGCCAAAATTGAAGAAACT 420
ACCCCGCACGATTTCATTGAACACTTCCTCTCCAAAATG 2810
                                                                                                                                                                                                                                          AGCCGCCTGCAGCTGCGGGGGCCACTTGCATGTTCGTGGCCTCTAAGATGAAGGAGAC- 2653
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
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Pred. No. 1.1;
0; Mismatches 162;
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Search completed: January 21, 2002, 00:20:01 Job time: 2935 sec

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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Perfect score:
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927
1 ATGGCAGAGGAAAATCTAGA......CTTATACACATCTTTCTTAA 927
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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BG726093 AW036252	BE642779 AV527915 AW042725	AI728683 CNS00U5S BE442681	AW507921 AI728767 BI306295	ID BG129531
	BE642779 Cr12_6_P2 AV527915 AV527915 AW042725 ST24F07 P	AI728683 BNLGHill3 AL090574 Arabidops BE442681 WHE1101 A		Description BG129531 EST475177

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WHE096 IP1_26 Sq75b0 SGT474 EST474		3 EST50717 6 EST48690 2 EST50767 2 EST50767 4 18H7 Pin 1 EST51273 2 EST52827 7 EST52827 6 EST52826 6 EST51118 0 EST51118 9 EST32184 4 EST52908 3 EST52908

ALIGNMENTS

RESULT

	source	FEATURES				COMMENT	JOURNAL	TITLE		AUTHORS	REFERENCE				ORGANISM	SOURCE	KEYWORDS	VERSION	ACCESSION		DEFINITION	LOCUS	BG129531
/organism="Lycopersicoh esculentum" /cultivar="TA496" /db_xref="taxon:4081" /clone="cToF24H8" /clone_lib="tomato shoot/meristem" /tissue_type="shoot/meristem" /tissue_type="shoot/meristem" /dev_stage="developing shoots from 4-6wks old plants" /lab_host="SOLR" /note="Vector: pBluescript SK(-); Site_1: EcoR1; Site_2:	1673	Location/Qualifiers	Email: http://www.genome.clemson.edu/orders/index.html.	Clemson University 100 Jordan Hall, Clemson, SC 29634, USA	Clemson University Genomics Institute	Contact: CUGI	Unpublished (2001)	Generation of ESTs from tomato shoot/meristem tissue	Hansen, C., Ronning, C. and Tanksley, S.	van der Hoeven, R., Bezzerides, J., Sun, H., Cho, J., Utterback, T.,	1 (bases 1 to 673)	Turoportroiros Turoportroiros	Asteridae, emasterida I. solamales, solamaceae, solamim.	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta: Magnoliophyta: endicotyledoms: core endicots:	Lycopersicon esculentum	tomato.	EST.	BG129531.1 GI:12629719	BG129531	cTOF24H8 5' sequence, mRNA sequence.	ot/meristem Lycopersicon escul	BG129531 673 bp mrNA EST 31-JAN-2001	

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RESULT
AW507921
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            83
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TGTGTTTGAGGCTAAATCAGTCCAAAGAATGG-AGCTTTTGGTGTTGAACAATTGAAAAT 523
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CAAAATTGAAGAAACTGAAGTTCCAATGTTGATAGATCTTCAGGTTGGAGATCCTCAGTT 464
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GCCTAGTGGCAAAGGTTGGATATTGCAGTTGTTGGCTGTGGCTTTATCATTGGCAGC 404
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                                                                                                                                                                                                                                                                                                                            CATCAGTGCCT
                                                                                                                                                                                                                                                                                                                                                                                             TAATCAAAGGTATTGACTTCTTGGAATTCAGGTCTTCTGAAATTGCAGCAGCAGCAGCAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  415;
                                             Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae
                                                                                                                                      EST.
                                                                                                                                                                                                     si47a06.y1 Gm-r1030 Glycine max cDNA clone GENOME SYSTEMS CLONE ID:
Gm-r1030-2027 5' similar to TR:P93103 P93103 CYCLIN-D LIKE PROTEIN.
 Shoemaker, R.,
                                 Glycine.
                                                                                                    Glycine max
                                                                                                                                                    AW507921.1 GI:7145999
                                                                                                                                                                                                                                           AW507921
                                                                                                                                                                                    mRNA sequence.
                 (bases 1 to 631)
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89 c 158 g 225 t
                                                                                                                                                                                                                                                                                                                            612
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 Keim, P.,
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Vodkin,L.,
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Erpelding, J.,
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Qγ 밁 Ω DЬ Qy DЬ Qy дb Qy Db

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FEATURES
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JOURNAL
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Matches 331; Conserv
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                                                                                                                           CAGTCCAAAGAATGGAGCTTTTTGGTGTTTGAACAAATTGAAATGGAGATTGAGAGCAATAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                          TAGCAATGAACTACTTGGATCGATTCTTATCGGTTCATGATTTGCCTAGTGGCAAAGGTT 361
                          CTCCATGCTCATACATAAGATATTTCCTGAGAAAGATGAGTAAATGTGATCAAGAACCAT
                                                                                                                                                                                                   AAGTTCCACTCTCTTGATTTGCAGGTGGGTGAATCGAAGTTTTTATTTGAGGCTAAAA 188
                                                                                                                                                                                                                                                     AAGTTCCAATGTTGATAGATCTTCAGGTTGGAGATCCTCAGTTTGTGTTTTGAGGCTAAAT 481
                                                                                                                                                                                                                                                                                                       GGACAATGCAATTGTTGGCTGTGGCGTGTTTATCTCTAGCAGCCAAATTAGATGAGACAG
                                                                                                                                                                                                                                                                                                                                                         GGATATTGCAGTTGTTGGCTGTGGCTTGTTTATCATTGGCAGCCAAAATTGAAGAAACTG
CTCCTTTCACCTTCCTTGATTACTTTCTTTGTAAGAT---CAACGATGATCAAAGTCCAT
                                                                                                 TATCTATAAATTACTTGGACCGATTCCTCTTTGCATATGAATTACCGAAGGGAAGAGTTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A., Bolla,B., Marra,M., Hillier,L., Kucaba,T., Martin,J., I Wylie,T., Underwood,K., Steptoe,M., Theising,B., Allen,M., E,Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., R., Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., N., R., Waterston,R. and Wilson,R., Pape,D., Cardenas,M., N., Pape,D., Cardenas, M., N., Waterston,R. and Wilson,R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: est@watson.wustl.edu
This clone is available through: Genome Systems, Inc. 4633 World
This clone is available through: Genome Systems, Inc. 4633 World
Parkway Circle St. Louis, Missouri 63134 For further information
call: (800) 430-0030 or (314) 427-3222 FAX:(888) 919-3324 or (314)
427-3324 or contact: clones@genomesystems.com or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Tel: 314 286 1800
Fax: 314 286 1810
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   synthesized from mRNA using a poly(dT) sequence with a NotI restriction site. Sall linkers adapters were ligated to the blunt-ended cDNA fragments followed by NotI digestion. The cDNA fragments were directionally cloned into the NotI-Sall restriction site of the pSPORT1 vector. The ligated cDNA fragments were transformed into E. coli ElectroMax DH10B host cells. This library was constructed by Dr. Lila Vodkin and Dr. Anu Khanna. Note that Gm-r1030 is a re-rack of Gm-c1007."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="Vector: psport1; Site_1: Sal1; Site_2: Not1; This cDNA library was constructed from mRNA isolated from immature cotyledons of greenhouse grown plants (individual seed fresh weight of 100-300mg). The library was prepared using the Life Technologies pSuperScript cDNA library construction kit. Complementary DNA was
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Glycine max"
/db_xref="taxon:3847"
/clone="GENOME SYSTEMS
/clone_lib="Gm-r1030"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /lab_host="DH10B"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 202.4;
Pred. No. 5.2
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nes 171;
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305 CAATGAACTACTTGGATCGATTCTTATCGGTTCATGATTTGCCTAGTGGCAAAGGTTGGA 364
                                                          331
                                                                                                                                                               185
                                                                                                                                                                                                  214
                                                                                                                                                                                                                                125 AGAGTGAGGAGATTATCATGGAGATGGTGGAGAAGGAGGAGCAGCATTTGCCAAGTGATG 184
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                                                                                                                                                              AAAGTGATGATCGAATCAAAGAGATGGTTGAAAAGGAGGTGGAGCATTTGCCTGAAGATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AGAGACTATTGAAGTGTGTTCAAATGAT 510
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                                                                       TCAATTGGATTTGGAAGGCTTGTGAAGTACACCAGTTTGGACCATTGTGTTTTTTGCTTAG 304
                                                                                                                            ATTATCTCAAGAGACTGAGAAGTGGGGATTTGGACTTGAGTGTT---ACGAAAGAGGCTC
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                                                     TTGATTGGATTTGGAAGGCTTCTGCTTATTACGGTTTTGGACCTTTGAGTCTTTGCCTAT 390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gossypium hirsutum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Malvales; Malvaceae; Gossypium.

1 (bases 1 to 512)
Blewitt,M., Matz,E.C., Davy,D.F. and Burr,B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Brookhaven National Laboratory
Upton, NY 11973, USA
Tel: 516-344-336
Fax: 516-344-3407
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AI728767 512 bp mRNA EST 11-JUN-BNLGH111561 Six-day Cotton fiber Gossypium hirsutum cDNA to (AJ011892) cyclin D2.1 protein [Nicotiana tabacum], mi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ESTs from developing cotton fiber Unpublished (1999)
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                                                                                                                                                                                                                                                                                                                                                                                   146
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primer: T3 Primer.
                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Gossypium hirsutum"
/Gultivar="Acala Maxxa"
/db_xref="taxon:3635"
/clone_lib="5ix-day Cotton fiber"
/tissue_type="immature fiber"
/dev_stage="5ix days post anthesis"
/lab_host="XL1-Blue"
                                                                                                                                                                                                                                                                                                                                                                               /note="Vector: pBluescript II KS+"
86 c 113 g 167 t
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Pred. No. 2.1e-33;
D; Mismatches 73;
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                                                                                                                                                                                                                                                                                                               Local Similarity
AACTACTTGGATTCTTATCGGTTCATGATTTTGCCTAGTGGCAAAGGTTGGATATTG
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                                                                                              TGGATTTGGAAGGCTTGTGAAGTACACCAGTTTGGACCATTGTGTTTTTGCTTAGCAATG
                                                                                                                                      CTGGAGAAGCTGGAGCTCGGTGGATTGGA----GTGTTCTTGGAGGAAAGATGCCATTGAT
                                                                                                                                                                                                                TGGATTTGCAAGGTCCATTCCTACTACAACTTTGGACCACTCAGCCTTTACCTCGCAGTG
                                                                                                                                                                          ATCAAGAGACTTAGAAGTGGAGATTTGGATTTGAATGTTGGAAGAAGAGATGCCCTCAAT 249
                                                                                                                                                                                                                                                                                               322;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BI306295 790 bp mRNA EST 20-JUL-2001 NL_4_BI2 Drought stress (leaf) Oryza sativa cDNA clone NL_4_BI2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    mRNA sequence.
BI306295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Department of Plant Sciences, School of Life Sciences University of Hyderabad P.O. Central University, Hyderabad-500 046, A.P, India Tel: 0091-40-3010265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Unpublished (2001)
Contact: Reddy AR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Insert Length: 790 Std Error: Plate: 4 row: B column: 12 Seg primer: GTAAAACGACGGCCAGTG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               stressed rice (Oryza sativa L.cv Nagina 22)
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Novel EST enrichment with normalized cDNA libraries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Oryza sativa
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: arjulsl@uohyd.ernet.in
Insert Length: 790 Std Erro
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ehrhartoideae; Oryzeae; Oryza.
1 (bases 1 to 790)
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                                                                                                                                                                                                                                                                                             Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Oryza sativa"
/cultivar="Nagina 22 (indica sub sp)"
/db_xref="taxon:4530"
/db_xref="taxon:4530"
/clone="NL_4_B12"
/clone=lib="Drought stress (leaf)"
/tissue_type="Entire leaf tissue"
/dissue_type="35 day-old seedlings"
/note="Organ: Leaf; Vector: T7T3Pac; ESTs from normalized leaf cDNA Library from drought stressed seedlings "
239 c 179 g 150 t
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58.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TCTTTCATCGGCTACTTCCTGGACAAGTTCAATGAAGGGAAGC---CGCCGAGCTACACG
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Gossypium hirsutum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids I; Malvales; Malvaceae; Gossypium.
                                                                                                                                                                                                                                                                                                                                                                                            Brookhaven National Laboratory Upton, NY 11973, USA Tel: 516-344-3396
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BNLGHill316 Six-day Cotton fiber Gossypium hirsutum cDNA 5' to (AJ011892) cyclin D2.1 protein [Nicotiana tabacum], mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Ben Burr
Biology Department
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Blewitt,M., Matz,E.C., Davy,D.F. and Burr,B. ESTs from developing cotton fiber
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AI728683.1 GI:5047535
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                                                                                                                                                                                                                                                                                                                                                                              Fax: 516-344-3407
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                                                                                                                                                                                                                                                                                                                                            primer:
                                                                                                                                                          156
                                                        Conservative
                                                                                                                                                                                       /db_xref="taxon:3635"
/clone_lib="Six-day Cotton fiber"
/tissue_type="immature fiber"
/dev_stage="Six days post anthesis"
/lab_host="XL1-Blue"
                                                                                                                                                         /note="Vector: pBluescript II KS+" 101 c 117 g 186 t 2
                                                                                                                                                                                                                                                                           /organism="Gossypium hirsutum"
/cultivar="Acala Maxxa"
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                                                   Score 153; DB 10;
Pred. No. 3.4e-29;
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TITLE
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Best Local
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                                               ATGGCTCAGACTTATGTTCACAAACACCCCAATGGGGTTTTAGAAGTATCGGCTTGTTGTT
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CNSO0U5S 381 bp DNA GSS 28-JUN-1999
Arabidopsis thaliana genome survey sequence SP6 end of BAC T6D11 of TAMU library from strain Columbia of Arabidopsis thaliana, genomic
                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (25-JUN-1999) Genoscope - BP 191 91006 EVRY cedex - FRANCE (E-Web : www.genoscope.cns.fr)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Genoscope.
Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Unpublished
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                                                                                                                                                                                       Similarity
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                                                                                                                                                                                                                                                               /db_xref="taxon:3702"
/clone_lib="TAMU"
/clone="T6D11"
/note="end: SP6"
a 42 c 69 g
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                                                                                                                                                                                                                                                                                                                                             /organism="Arabidopsis
/strain="Columbia"
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                                                                                                                                                                                      16.1%; 92.4%;
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                                                                                                                                                                         Mismatches
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                                        286 CCATTGTGTTTTTGCTTAGCAATGAACTACTTGGATCGATTCTTATCGGTTCATGATTTG 345
_
CCGTTGACTGCGGTCCTGTCTGACTACCTTGATAGGTTCCTCTCCGTCTATCCCCTT 60
                                                                                           263;
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BE442681
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1 (bases 1 to 621)

Anderson,O.D., Chao,S., Choi,D.W., Close,T.J., Fenton,R.D., Han P.S., Hsia,C.C., Kang,Y., Lazo,G.R., Miller,R., Nguyen,H.T., Rausch,C.J., Seaton,C.L., Tong,J.C. and Zhang,D.

The structure and function of the expressed portion of the wheat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BE442681 621 bp mRNA EST 25-JUL-2000 WHE1101_A09_A172S Wheat etiolated seedling root normalized cDNA library Triticum aestivum cDNA clone WHE1101_A09_A17, mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US Department of Agriculture, Agriculture Research
West Area, Western Regional Research Center
800 Buchanan Street, Albany, CA 94710, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence have been trimmed to remove vector quality sequence with phred score less than Seq primer: Stratagene SK primer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Unpublished (2000)
Contact: Olin Anderson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          genomes - Normalized root cDNA library
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooldea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Triticum aestivum
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              oandersn@pw.usda.gov
                                                                                                                                                                                                                                                                                                                                                                                                     dishes. Roots were harvested. The tissue, total RNA, poly(A) RNA were prepared, a cDNA library was made i TJ Close lab (Choi, Close, Fenton) at the University California, Riverside. The cDNA clones were in vivo excised to give pBluescript phagamide hafacrants.
                                                                                                                                                                                                                                  excised to give pBluescript phagemids before normalization was carried out. The mass excision of phagemid library and normalization were done in HT Ng lab by D. Zhang at Texas Tech Univeristy. Normalizati protocol used was that of Soares. Plasmid DNA preparations and DNA sequencing were performed in the Anderson lab (all other authors)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               pBluescript SK; Site_1: EcoRI; Site_2: XhoI; Seeds were surface-sterilized, germinated and grown aseptically in the dark at room temperature on filter paper with water, nystatin and cefotaxime in covered crystallization
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /dev_stage="Five day old etiolated seedling"
/lab_host="E. coli DH10B"
/note="Vector: Lambda Uni-ZAP XR, excised phagemid
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/db_xref="taxon:4565"
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/cultivar="Chinese Spring"
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                                                                                                                  16.1%;
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Pred. No. 3.4e-28;
0; Mismatches 168
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TCTGTTTCTGGAGA 719
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BE642779 813 bp mRNA EST 01-SI Cri2_6_P20_SP6 Ceratopteris Spore Library Ceratopteris cDNA clone Cri2_6_P20 5', mRNA sequence.
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Eukaryota; Viridiplantae;
Filicophyta; Filicopsida;
                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Roux SJ
                                                                                                                                                                                                                                                                                                                                                                                                                                       Expressed sequence tags 
Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Chatterjee, A., San Miguel, P., Stout, S.(
Expressed sequence tags of cDNA clones
                                                                                                                                                                                                                                                                                                                 Email: sroux@uts.cc.utexas.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ceratopteris richardii.
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                                                                                                                                                                                                                                                                              primer: SP6
                  196
                  a
                                               /cell_type="Spore"
/dev_stage="20 hours after germination initiation"
/dev_stage="20 hours after germination initiation"
/note="Vector: pcMVSPORT6; EST sequence from cDNA library
cDNA library constructed from mRNA isolated from C
richardii spores that had developed for 20 hours after
                                                                                                                       /tissue_type="Gametophyte"
/cell_type="con--"
                                  their
                                                                                                                                                      /clone="Cri2_6_P20"
/clone_lib="Ceratopteris
                                                                                                                                                                                         /cultivar="Brogn"
/db_xref="taxon:49495"
                                                                                                                                                                                                                                                              Location/Qualifiers
                                                                                                                                                                                                                          organism="Ceratopteris richardii"
                  169
                                                                                                                                                                                                                                                                                                row: P
                germination had been initiated by white light.
9 c 191 g 257 t
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                                                                                                                                                                                                                                                                                                column:
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                                                                                                                                                                                                                                                                                                                                                                      Austin,
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Stout,S.C., Banks,J. and Roux,S.J. NA clones from a C. richardii library
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Query Match

13.3%;

Score 123.6;

DВ

10;

Length 813;

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RESULT
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                                                                                         BASE COUNT
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                                                                                                                                                                                                                                                                                                                                                                                                                                   Asamizu, E., Nakamura, Y., Sato, S. and Tabata, S.
A large scale analysis of cDNA in Arabidopsis thaliana: Generation of 12,028 non-redundant expressed sequence tags from normalized and size-selected cDNA libraries
DNA Res. 7, 175-180 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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AV527915 Arabidopsis thaliana
old Arabidopsis thaliana cDNA
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Kazusa DNA Research Institute
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Contact: Erika Asamizu
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                                                                                                         125
     Conservative
                                                                                                                                                                                                                                                                                                                               1532-3, Kisarazu, Chiba 292-0812, Japan
1: asamizu@kazusa.or.jp, URL:http://www.kazusa.or.jp/en/plant/.
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                                                                                                                                                                                             /clone_lib="Arabidopsis thaliana aboveground
six-week old"
                                                                                                                                                                                                                             /organism="Arabidopsis
/strain="Columbia"
/db_xref="taxon:3702"
/clone="APZ47c12R"
                                                                                                                                       /note="Vector: pBluescriptII SK-;
                                                                                                                                                           /dev_stage="two
                                                                                                                                                                           /tissue_type="aboveground organs
                                                                                                                                                                                                                                                                                                             Location/Qualifiers
                   12.5%;
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0; Mismatches
                   Score 116; DB 10; Pred. No. 1.3e-19;
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   Mismatches
                                                                                                                                                             to six-week old"
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                                   Length 478;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AW042725 596 bp mRNA EST 18-SEP-1999 ST24F07, Pine TriplEx shoot tip library Pinus taeda cDNA clone ST24F07, mRNA sequence.

AW042725
                                                                                                                                                                                                                                                                                                                                                                                                                               Dept. of Forestry, NC, NC, 27695-8008
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Whetten,R.W., Kinlaw,C.S., Retzel,E.
The Pine Gene Discovery Project
Unpublished (1999)
Contact: Ross Whetten
                                                                                                                                                                                                                                                                                                                                                Email: rosswhet@unity.ncsu.edu
Seq primer: 5' lambda TriplEx2 Sequencing
                                                                                                                                                                                                                                                                                                                                                                                         Fax: 919-515-7801
                                                                                                                                                                                                                                                                                                                                                                                                                Tel: 919-515-7800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Forest Biotechnology Group
North Carolina State University
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Spermatophyta; Coniferopsida; Coniferales; Pinaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pinus taeda
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                 135
      /Clone_lib="Pine TriplEx shoot tip library"
/lab_host="E. coli BM25.8"
/lab_host="E. coli BM25.8"
/note="Organ: shoot tips: Vector: Lambda TriplEx; Site_1: SfiI (A); Site_2: SfiI (B); Shoot tips (approx. 2 cm from apex) were collected during the spring, frozen and used for mRNA isolation. The SMART-PCR method (Clontech) was used to prepare a library from 1 ug total RNA, using the Lambda TriplEx vector. Plasmid subclones in pTriplEx were recovered by cre-lox excision in E. coli strain BM25.8 and sequenced from the 5' end."

35 a 152 c 153 g 151 t 5 others
                                                                                                                                                                                                                                           /db_xref="taxon:3352"
/clone="ST24F07"
                                                                                                                                                                                                                                                                                    /organism="Pinus taeda"
                                                                                                                                                                                                                                                                                                                             location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                     State University, 6113 Jordan Hall, Raleigh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sederoff, R.R
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Pinus; Pinus.
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Matches Query Match

Best Local Similarity Matches 228; Conserv

Conservative

0;

Mismatches

Indels Length

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Gaps

1:

Pred. No.

1.7e-1

Score 111.8; DB 10;

596;

12.1%; 56.3%;

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JOURNAL COMMENT
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                                                                                                                                                                                                                                                                                                                                                                                                                          מ מ
                                                                                                                                                                                                                                                                                       Unpublished (1999)
Contact: Shoemaker R/Public Soybean EST Project
Public Soybean EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, Parkl: 314 286 1800
                                                                                                                                                                                                                                                                                                                                                                                                                          Shoemaker,R., Keim,P., Vodkin,L., Erpelding,J., Coryell,V., Khanna,A., Bolla,B., Marra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C. Wylie,T., Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers,Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurl,R., Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R., Waterston,R., and Wilson,R.
                                                                                                                              Email: est@watson.wustl.edu
This clone is available through: Genome Systems, Inc. 4633 World
Parkway Circle St. Louis, Missouri 63134 For further information
call: (800) 430-0030 or (314) 427-3222 FAX:(888) 919-3324 or (314)
427-3324 or contact: clones@genomesystems.com or
info@genomesystems.com web site: www.genomesystems.com
High quality sequence stop: 412.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PROTEIN. ;, mRNA sequence. BG726093 BG726093.1 GI:14011162 EST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BG726093 498 bp mRNA sae06h09.yl Gm-c1055 Glycine ID: Gm-c1055-4578 5' similar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Spermatophyta; Magnoliophyta; Embridae; Papallionoideae; Phaseoleae
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Glycine max
                                                                                                                                                                                                                                                                                                                                                                                                          Public Soybean EST Project
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                                                                                                                                                                                                                                                                         314 286 1800
314 286 1810
                    /clone="GENOME SYSTEMS CLONE
/clone_lib="Gm-c1055"
                                                        /organism="Glycine max"
/db_xref="taxon:3847"
  /tissue_type="Mature seed
                                                                                                                Location/Qualifiers
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max cDNA clone GENOME SYSTEMS CL
to TR:Q9ZRX9 Q9ZRX9 CYCLIN D2.1
pods,
                                                                                                                                                                                                                                                                                                             St. Louis, MO 63108, USA
                                      ID: Gm-c1055-4578"
greenhouse grown"
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/lab_host="DH10B"
/note="Vector: pBluescript II SK+; Site_1: EcoRI; Site_2: Anote="Vector: pBluescript II SK+; Site_1: EcoRI; Site_2: XhoI; The cDNA library was constructed from mRNA isolated from mature seed pods of greenhouse grown plants prior to senescence for the cultivar KP1. Complementary DNA was synthesized from mRNA using a primer consisting of a poly(dm) sequence with a XhoI restriction site. EcoRI adapters were ligated to the blunt-ended cDNA fragments followed by XhoI digestion: The cDNA fragments were directionally cloned into the EcoRI-XhoI restriction site of the pBluescript vector. The ligated cDNA fragments were transformed into DH10B host cells (GibcoBRL). This library was constructed in the laboratory of Dr. Randy Shoemaker."
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Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                            Unpublished (1999)
Contact: CUGI
Clemson University Genomics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AW036252 558 bp mRNA EST 18-MAY-2001 EST2778331 tomato seed, TAMU Lycopersicon esculentum cDNA clone cLEED2020 similar to cyclin, putative, mRNA sequence.

AW036252
                                                                                                                                                                             Email: http://www.genome.clemson
5 prime sequence.
                                                                                                                                                                                                                                                                                                                                                  C.L., Nierman,W., Frase,S.D. and Giovannoni,J. Generation of ESTs from
                                                                                                                                                                                                                                                                                                                                                                                                    Alcala,J., Vrebalov,J., White,R., Matern,A.L., Vision,T., Liang,F., Upton,J., Ronning,C.M., Craven,M.B., Fujii,C.Y.,C.L., Nierman,W., Fraser,C.M., Venter,J.C., Martin,G.B.,
                                                                                                                                                                                                                            Clemson University
100 Jordan Hall, Clemson,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Spermatophyta; Solanales; Solanaceae; Solanum;
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                                            /organism="Lycopersicon
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/db_xref="taxon:4081"
/clone="cLEE2D20"
/clone_lib="tomato seed,
                                                                                                                                                   Location/Qualifiers
                                                                                                                              . 558
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Pred. No. 1.9e-18;
                                                                                                                                                                                                                                                                                                                                                          tomato seed tissue
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                                                                                                                                                                                                                                                                                 Institute
                                                                                                                                                                                                                               29634, USA
                                                                                                                                                                                                                                                                                                                                                                                                       Venter, J.C., Martin, G.B., Tanksley
                                                                                                                                                                                                     .edu/orders/index.html
                                                                                                 esculentum"
  TAMU"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ACTCAAGTTCCCCCTTCTTGACTTCCAAGTGGAGGATGCAAAATATGTGTTTGAGGCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CCATGGATGACTCAACTTGCTGCTGTCACTTGTCTTTAGCGGCTAAAGTTGAAGAA
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                                                              Email: kate@mail.bio.tamu.edu
M393960e TIGR sequence name: MTECC60TK More
available at: www.medicago.org
Seq primer: SKmod (CTA gAA CTA gtg gAT CC).
                                                                                                                                                                                                                                                                                                                                              VandenBosch, K., Endre, G., Hur, J., Beremand, P., Town, C.D., C.L., Craven, M.B., Cho, J. and Fraser, C.M.
ESTs from roots of Medicago truncatula 72 h after Rhizobi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       mRNA sequence.
BG645553
BG645553.1 GI:13780665
                                                                                                                                                           Tel: 409 845 7707 Fax: 409 845 2891
                                                                                                                                                                                                        College Station, TX 77843-3258,
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I; Fabales; Fabaceae; Papillonoideae; Trifolieae;
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EST507172 KV3 Medicago
                                                                                                                                                                                                                                Texas A&M University
                                                                                                                                                                                                                                                                                Contact: VandenBosch K
                                                                                                                                                                                                                                                                                                      Unpublished (2001)
                                                                                                                                                                                                                                                                                                                         inoculation,
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                                                                                                                                                                                                                                                      Department of Biology
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                                                                                                                                                                                                                                                                                                                                                                                                                                              Medicago.
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/dev_stage="quiescent seed"
/lab_host="XL1-Blue MRF',"
                                           Location/Qualifiers
/organism="Medicago truncatula"
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RESULT 1 BG585146

DEFINITION LOCUS

BG585146 809 bp mRNA ES EST486909 MHAM Medicago truncatula/Glomus library cDNA clone pMHAM-22A23 5' end, mRN

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Best Local S
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                                    GCAGAGAGTACACTTTGACAACTCT 747
                                                                                                                                                 CCACTTCATAATTTCACGTGCTACAGAAATCATCTTATCTAATATCCAAGATGCTAGCTT
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TCCTAATTGGTCTTTTGTTAATCCT
                                                                        TCTTACTTACAGGCCATCATGCATTGCTGCAGCTGCCATACTCTCTGCAGCTAATGAAAT
                                                                                                            TTTGGAGTTTAGACCTTCTGAAGCTGCTGCTGTTGTCACTTTCTGTTTCTGGAGAATT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="Vector: pBluescript SK -; Site_1: EcoRI; Site_2: XhoI; cDNA was prepared from polyA+ enriched RNA. The cDNA was directionally ligated into the Unizap XR vector from Stratagene and packaged using Gigapack III Gold packaging extracts. Plasmids containing cDNA inserts were excised from the recombinant lambda-Zap phage using Ex-assist helper phage and propagated in XLOLR cells."
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/dev_stage="3 days post-inoculation with Sinorhizobium
meliloti"
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/db_xref="taxon:3880"
/clone="pKV3-46J23"
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50.7%;
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Pred. No. 6.1e-18;
0; Mismatches 302
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                                                                                                                                                     AGCAATGAACTACTTGGATCGATTCTTATCGGTTCATGATTTGCCTAGTGGCAAAGGTTG 362
                                                                                                                                                                                                              CATTGCATGGATTCTCAAGGTACATGAGTATTATGGATTTCAGCCGTTAACGGCGTACCT
                                                                                                                                                                                                                                                        CCTCAATTGGAATTTGGAAGGCTTGTGAAGTACACCAGTTTTGGACCATTGTGTTTTTTGCTT
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                                                                                                                                                                                                                                                                                                                                                                                    GGAAGAGGAGGAGTCGATTGCTTTTCATCGAGCACGAGTTCAAGTTTGTTCCTGGTTT 212
                                            GCCACTGCAACTTTTATCTGTTGCATGTTTGTCTTTAGCAGCAAAGATGGAGGAACCACT
                                                                                 GATATTGCAGTTGTTGGCTGGCTTGTTTATCATTGGCAGCCAAAATTGAAGAAACTGA 422
                                                                                                                             CTCCGTTAACTATATGGATCGGTTTTTGGATTCTCGACCTTTACCGGAATCAAATGGATG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Medicago truncatula/Glomus versiforme mixed Medicago truncatula/Glomus versiforme mixed Eukaryota; mixed EST libraries.

1 (bases 1 to 809)
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BG585146.1 GI:13600210
EST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Noble EST name: N3806196 TIGR sequence name: MTDCA12TK More information is available at: http://www.medicago.org Seq primer: SKmod (CTA gAA CTA gtg gAT CC).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Fax: 580-221-7380
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Glomus versiforme, 2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Harrison, M.J., Liu, J., Town, C.D., Van
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Samuel Roberts Noble Foundation O Sam Noble Parkway, Ardmore, OK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  194
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              from roots of Medicago truncatula after colonization with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     mjharrison@noble.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note-"Vector: pBluescript SK; Site_1: EcoRI; Site_2: XhOI; cDNA was prepared from polyA+ enriched RNA from roots harvested at 10, 17, 22, 31 and 38 days post-inoculation with Glomus versiforme. The cDNA was directionally ligated into the Unizap XR vector from Stratagene and packaged using Gigapack III Gold packaging extracts. plasmids containing cDNA inserts were excised from the recombinant lambda-Zap phage using Ex-assist helper phage and propagated in XLOLR cells."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /tissue_type="roots colonized with Glomus versiforme" /dev_stage="Roots harvested at 10, 17, 22, 31 and 38 post-inoculation with Glomus versiforme. The library made from a mixture of RNA from each of these stages.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /cultivar="Medicago truncatula genotype A17"
/db_xref="taxon:119092"
/clone="рмнам-22A23"
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Pred. No. 6.1e-18;
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                                                                                                                                                                                                                                                                                                                                                                                                                                         Department of Biology
Texas A&M University
College Station, TX 77843-3258,
Tel: 409 845 7707
Fax: 409 845 2891
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Medicago truncatula
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BG646052 810 bp
EST507671 KV3 Medicago
                                                                                                                                                                                                                                                                                                                                          available at: www.medicago.org
Seq primer: SKmod (CTA gAA CTA gtg
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: VandenBosch K
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VandenBosch,K., Endre,G., Hur,J:, Beremand,P.,,C.L., Craven,M.B., Cho,J. and Fraser,C.M. ESTs from roots of Medicago truncatula 72 h afi
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Medicago
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (bases 1 to 810)
     195
                                                                                                                                                                                                                                                                                                                                                                                                                         kate@mail.bio.tamu.edu
   a
           meliloti"
//lab_host="E. coli strain XLOLR"
//lab_host="E. coli strain XLOLR"
//note="Vector: pBluescript SK -; Site_1: EcoRI; Site_2:
//note="Vector: pBluescript SK -; Site_1: EcoRI; Site_2:
XhoI; cDNA was prepared from polyA+ enriched RNA. The cDNA
was directionally ligated into the Unizap XR vector from
Stratagene and packaged using Gigapack III Gold packaging
extracts. Plasmids containing cDNA inserts were excised
from the recombinant lambda-Zap phage using Ex-assist
                                                                                                                                                                      /tissue_type="Seedling roots"
/dev_stage="3 days post-inoculation with Sinorhizobium
meliloti"
helper phage and propagated in XLOLR 201 c 170 g 244 t
                                                                                                                                                                                                                                                 /organism="Medicago truncatula"
/cultivar="genotype A17"
/db_xref="taxon:3880"
/clone="pKV3-48G20"
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pkv3-48G20 5' enc
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Best Local Similarity 51.3
Matches 308; Conservative
                                                                                                                                                                                                                                                                                                                                                                                 423 AGTTCCAATGTTGATAGATCTTCAGGTTGGAGATCCTCAGTTTGTGTTTTGAGGCTAAATC 482
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                                                                                                                         663 TTTGGAGTTTAGACCTTCTGAAGCTGCTGCTGCTGTGTGCACTTTCTGTTTTCTGGAGAATT 722
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                                               723 GC 724
                                                                                              741 TCTTACTTACAGGCCATCATGCATTGCTGCAGCTGCCATACTCTCTGCAGCTAATGAAAT 800
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                267 CGACTACGTCTCAAGATTCCAATCTCGCTCTCGCAATCCA---GCACCAGAGAAGAAGC 323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              183 TGATTACATCAAGAGACTTAGAAGTGGAGATTTGGATTTGAATGTTGGAAGAAGAGATGC 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              207 GGAAGAGGAGGAGTCGATTGCTGTTTTCATCGAGCACGAGTTCAAGTTTGTTCCTGGTTT 266
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Search completed: January 20, 2002, 23:56:13 Job time: 3402 sec

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9b_P1: ATCD2
9b_P1: ATCD2
9b_P1: AC006592
9b_P1: ATCD1
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gb_p1:ATF12B17
gb_pat:A85057
gb_p1:NTA011892
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-DB=-GenEmb1 -OBMT=fastap -SUFFIX=rge -GAPOP=12 000 -GAPEXT=4.000
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-QGAPEXT=0.050 -XGAPOP=10.000 -XGAPEXT=0.500 -FGAPOP=6.000
-FGAPEXT=7.000 -YGAPOP=10.000 -YGAPEXT=0.500 -DELOP=6.000
-DELEXT=7.000 -START=1 -NATRIX=blosum62 -TRANGS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0
-ALIGN=15 -MODE=LOCAL -OUTFMT=pfs -NORM=ext -HEAPSIZE=500
-MINLEN=0 -MAXLEN=200000000 -USER=US09530209_@CGN1_1_6669
-NCPU=6 -LOPU=3 -LONGLOG -DEV_TIMEOUT=120 -WARN_TIMEOUT=30
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156 | ABO11479 Arabidopsis thaliana
1053 | AL353995 Arabidopsis thaliana
14 | A85057 Sequence 1 from Patent
14 | AJ011892 Nicotiana tabacum mRN
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150 | X83370 A.thaliana mRNA for cyc
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2 | AJ245415 Lycopersicon esculent

2 | AJ250398 Antirrhinum majus mRN

9 | AJ002590 Lycopersicon esculent

512 | AP003744 Oryza sativa chromo

11 | AL021961 Arabidopsis thaliana

861 | AL161584 Arabidopsis thaliana

12 | AL161584 Arabidopsis thaliana

13 | AL161584 Arabidopsis thaliana
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AJ131636 Arabidopsis thaliana
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! AJ132929 Medicago sativa cycD:
! AJ011776 Chenopodium rubrum ml
                           i AL132978 Arabidopsis thaliar
AJ132930 Medicago sativa cycli
X89475 X.laevis mRNA for cycli
X87581 D.reiro mRNA for cyclir
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AB008188 Pisum sativum cycDl m A85061 Sequence 5 from Patent X88864 M.sativa move.
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A85060 Sequence 4 from patent
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X83371 A thaliana mRNA for cy
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A85058 Sequence 2 from Patent
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Quality: 1583.00
Ratio: 5.140
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TITLE
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unclassified.

1 (bases 1 to 927)

A.J. and De.V.L.

A NOVEL WITOGENIC CYCLIN AND USES THEREOF

PALMETIC WO 9922002-A 1 06-MAY-1999;

ALMEIDE JANICE DE (BE); VEYLDER LIEVEN DE

LOCALLON/QUALIFIERS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  y2/ bp DNA
Sequence 1 from Patent WO9922002.
A96985
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A96985.1 GI:6780426
LCSQTPNGVLEVSACCFSFKTHDSSSSYTHLS"
148 c 223 g 287 t
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                                                                                                                                                                                                                                       organism="unidentified"
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4.7e-15
8.8e-15
2.0e-14
1.3e-14
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M83749 Mouse D-type cyclin
L09752 Rat cyclin D2 (VIN1)
AR034831 Sequence 3 from pat
196214 Sequence 51 from pat
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Quality: 1583.00 Length: 308
Ratio: 5.140 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000
Lignment_block: US-09-530-209A-2 x A96985 ...
Align seg 1/1 to: A96985 from: 1 to: 927

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VERSION
KEYWORDS
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                                                                REFERENCE
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LOCUS ATH131636
                                                                                                                                                                                                                    seq_name:
                                                                                                                           SOURCE
JOURNAL
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                              TITLE
                                                     AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GlyAspProGlnPheValPheGluAlaLysSerValGlnArgMetGluLe 167
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                                                                                                                                                                                                                                                        SerSerSerTyrThrHisLeuSer 308
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                                                                                                                                                                                                                     gb_p1:ATH131636
                                                      Arabidopsis thaliana AJ131636
        Unpublished
                 de Veylder,L., De Almeida Engler,J., Burssens,S., Manevski,A.,
Lescure,B., Van Montagu,M., Engler,G. and Inze,D.
A new D-type cyclin of Arabidopsis thaliana expressed during
lateral root primordia formation
                                                                                                                                  AJ131636.1 GI:4688614 cycd4.1 gene; D-type cyclin.
                                                                                                                                                                          mRNA for D-type cyclin
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Percent Similarity: 100.000
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de Veylder,L.
Direct Submission
Submitted (16-DEC-1998) De Veylder
Laboratorium voor Genetica, K.L. Le
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IDFLEFRPSEAAAAAVALSVSGELQRVHFDNSSFSPLFSLLQKERVKKIGEMIESDGSD
LCSQTPNQVLEVSACCFSFKTHDSSSSSYTHLS"
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/db_xref="taxon:3702"
118. .1044
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118. .1
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                   COMMENT
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AB011479 BA000015
AB011479.1 GI:20227777
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                                                                                                                                                               Structural analysis of Arabidopsis thaliana ch
Sequence features of the regions of 1,381,565
one physically assigned P1 and TAC clones
DNA Res. 5 (2), 131-145 (1998)
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                                                                                                                                                                                                                                                                              Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Genes encoding tRNAs are predicted by tRNAscan-SE (Sean Eddy, Washington University School of Medicine, http://genome.wustl.edu/eddy/tRNAscan-SE/)
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rllgfglseipktlwknadwttrokvlshkiakiavkldnahoelsnaivvaoatsto
mskrdpmrpynwvidamlakkereddsfkpogoolgenddyddelsnaivvaoatsto
mskrdpmrpynwvidamlakkereddsfkpogoolgenddyddelsnaturahlrhlrn
akdryrpkseyltyvtealvledtmknyerrdatgmkisfratrokkgnildsl
efmwrciikkolomvlavvmgimsaaillaeatillskldslesilissvksdellv
oafaryplvyncytyslfrigmlntysltprotssynlthicsmiaryappisyne
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                                                                                                                                                                                                                                                                                                                                                               /evidence=not_experimental
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complement(join(14356...14)
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                                                                                                                                     protein ATHB-5)"
                                                                                                                                                                                                                                                                                           sp|P46667"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        unknown protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FLPLRQSPETTALTSTRVVTSSVPQSLDEIFQRLKNRSVEHSPYLDDDDEV" complement(7165. .7617)
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/strain="Columbia"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              complement(9379. ..9466)
/note="gene_id:MNA5.3"
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CDS

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complement(31998. .32408)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /translation="MKQASSSSSRNSTSLTNRLKTIFKKAEELSILCAIEVCVIYYG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           similar to unknown protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 complement(25583. .26344)
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                                                                                                                                                                                                                                                                                                                                                                                                                sp|P05203"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  pir||T13016
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IKELKAKLNVEGYKGIEENGALKAVEANQSVMANNEVLELSHRSPSPPPHIPTDAPTS
ELAFEMFSIFPRTENFRDDPADSSDSSAVLNEEYSPNTVEAAGAVAATTVEMSTMGCF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LSNTVPHEFSSDFNQNPYGNAVGNISFSQDMFSSYDASSLLQTSSLPPLHNIPSSYCF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    \mathtt{RHANIKVLTKTQPRLLFKIINEFNSLGLSTLHLNLTTSKDMSLFTFSVKVEADCQLTP}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NHIAVERNRRKQMNHFLSILKSMMPLSYSQPNDQASIIEGTISYLKKLEQRLQSLEAQ
LKATKLNQSPNIFSDFFMFPQYSTATATATATASSSSSSHHHKRLEVVADVEVTMVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /translation="MMFQQDYPHGFSLVETSLSYEMLDYFQNIVVSNSEDVASQQNSI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /evidence=not_experimental
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qene_id:MNA5.5"
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                                                                                                                                                                                                                                                                                                                                                                              codon_start=1
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                                                                                 to unknown protein"
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IA5.9
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CDS

CDS

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NSVQPVLSGVAVGSGWQSYVAYINLGCYYCIGVPLGFLMGWGFKLGVMGIWGGMIFGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                             codon_start=1/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6. .35375,35475.
.37054,37141. .
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.37394,
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Quality: 1294.00 Ratio: 4.201 nilarity: 42.778 to reverse of: AB011479 Percent Identity: Length: Gaps: from: 1 to: 88356 42.500 720 7

Align seg 1/1 US-09-530-209A-2 x AB011479/rev Percent Similarity:

roGlnMetGlyPheSerGlnSerGluSerGluGluIleIleMetGluMet TGATGATGAGGGCATGATTGTTGACGAAACTCCGATTGAAATTTCGATTC 50 55550

ValGluLysGluLysGlnHisLeuProSerAspAspTyrIleLysArgLe GTGGAGAAGGAGCAGCATTTGCCAAGTGATTACATCAAGAGACT 67 55450

55500

84 55400

GGATTTGGAAGGTCTGATTCTCTATTTGATTTTGATTTCTGGTTTTGAAA 55350 rpIleTrpLys..... 87

TTTGGATGTTGATTGGATGATCTGTATAAGCTCAAATTGTGAAA 55300 87

87

TCTATTAGATCAGAGGCTTATGCAGAACAGATAGAGAGGTTTTGTCTTAA 55200 AGCACAATCCTTTTGATGAATGATCTGAACATAAAGAGTGTGTTGCTATG 87 55250

CDS

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99 55049	heLeuSerValHisAspLe CTTATCGGTTCATGATTT	115 55000
115	Pro	116
54999	TAAGTTCACATTGGTTAAACTAAAAGATTGATAATGTTTTTAGCC	54950
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117 54899	TG1YLYSG1YTTPI1eLeuG1nLeuLeuAlaVa1A1aCySLe 	131 54850
131 54849	laalaLysileGluGluThrGluValProMetLeuileAsp. 	147 54800
148 54799	LeuTranscricgttaaattgtcgagatgttctattcgacc	148 54750
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	GerArgSerLeuGlnValIl 	217 54500
21	— G	217
9	GTGAAAAAAAAGTCTTTCCTTTATGTTTTATTTTCTTGACCACTTTT	4
217 54449	ŢŢŢŢŢŢŢĊŢĊŢŢŢŢŢŢŢŢŢŢŢŢŢŢŢŢŢŢŢŢŢŢŢŢŢŢŢŢŢ	217
218	GlyIleAspPh	222
54399	TTGGATTAAAATGGTGGTTGTGTCGAGTGAGCAGGTATTGACTTTT	54350
222	uGluPheArgProSerGluAlaAlaAlaAlaAlaIalaLeuSerValSerG	239
23	yGluLeuGlnArqValHisPheAspAsnSerSerPheSerProLeuPh	5

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306 53500	laCysCysPheSerPheLysThrHisAspSerSerSerSerTyrThrHis 	290 53549
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273 53600	GluArgValLysLysIleGlyGluMetIleGluSerAs	261 53649
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260	SerLeuLeuGlnLvs	256
54250		54299

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JOURNAL REFERENCE
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                                                  intron
                                                                                                                                                          intron
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

1 (bases 1 to 113053)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Information on performance of analysis and a more detailed annotation of this entry and other sequences of chromosomes 3, 4 and 5 can be viewed at: http://www.mips.biochem.mpg.de/proj/thal/.
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AL353995.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mayer,K.F.X.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bevan, M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Arabidopsis thaliana
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (bases 1 to 113053)
                                                                                                                                                                                                                  SYSSIEQUILBSIGWERY FSGDSDLIQY HKRSSIDLISLPRDFSKFNSVYMYDIVVKN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          complement(join(447...575,662...796,901...1140,1493...1661,
1772...2259,2348...2458,2537...2925,3285...3440,3940...4104,
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                                                                                                                                                            .661)
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83000	GUTTTTGAGTTATGGGGTTATGGACTTTTGGGGTTAGAAATGATTGAT	10058
л . Л		n 1
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86 82750	yAspLeuAspLeuAsnValGlyArgArgAspAlaLeuAsnTrpIleTrp. ::: AGATTTGGATTTCAATGTCAGAATCCAAGCCCTTGGTTGGATTTGGA	70 82704
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                                                                                                                                ACCESSION
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                                                                                                                                                                                                                                                                                                                             TCTCTTTCT 84247
                                                                                                                                                                                                                                                                                           HisLeuSer 308
                                                                                                                                                                                                                                                                                                                                                                                                  AAGTTCAAGTTCACAAACACCAAATAATACAGTCTTACAATTTAAGAGTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 uLeuGlnArgValHisPheAspAsnSerSerPheSerProLeuPheSerL
                                                                                                                                                                                                                                                                                                                                                                                                                              rAspLeuCysSerGlnThrProAsnGly...ValLeuGluValSerAlaC
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common tobacco.

Nicotiana tabacum

Nicotiana tabacum

Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Spermatophyta; Magnoliophyta; eudicotyledons; Nicotiana.
                                                                                                                                Sequence 1 from Patent A85057
                                                                                                                A85057.1 GI:6733798
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182 ProCysSerTyrIleArgTyrPheLeuArgLysMetSerLysCysAspG1 198
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                                                        etGluLeuLeuValLeuAsnLysLeuLysTrpArgLeuArgAlaIleThr 181
                                                                                                                                                                                                           TCACTTGCAGCCAAAATGGAAGAAATTAATGTTCCTTTGACTGTTGATTT
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PLANTS WITH MODIFIED GROWTH
PLANTS WITH MODIFIED GROWTH
PATENT: WO 9842851-A 1 01-OCT-1998;
PATENT: WO 9842851-B 101-OCT-1998;
MURRAY JAMES AUGUSTUS HENRY (GB); UNIV CAMBRIDGE TECH
LOCATION/Qualifiers
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids I; Solanales; Solanaceae; Nicotiana.
I (bases 1 to 1284)
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Direct Submission
Submitted (07-OCT-1998) Murray J.A.H., Institute of Biotechnology,
University of Cambridge, Tennis Court Road, Cambridge, CB2 1QT, UK
2 (bases 1 to 1284)
Sorrell,D.A., Combettes,B., Chaubet-Gigot,N., Gigot,C. and
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AJ011892.1 GI:4160297
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/codon_start=1
/product="cyclin D2.1 protein"
/protein_id="CAA09852.1"
/db_xref="GI:4160298"
                                                                                                                                                             /gene="CycD2.1"
                                                                                                                                                                                                                                        /gene="CycD2.1"
                                                                                                                                                                                                                                                                                                              /cell_line="Bright Yellow 2 (BY-2)"
/dev_stage="exponentially growing company of the company of 
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/db_xref="taxon:4097"
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                                                                                                                                                                                                                                                                                                                   98 sPheCysLeuAlaMetAsnTyrLeuAspArgPheLeuSerValHisAspL 115
                                                                                                                                                                                                                                                                                                                                                                                                                    82 LeuAsnTrpIleTrpLysAlaCysGluValHisGlnPheGlyProLeuCy
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                                                                              uGlnValGlyAspProGlnPheValPheGluAlaLysSerValGlnArgM
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                                                                                                                                                                                                                    etGluLeuLeuValLeuAsnLysLeuLysTrpArgLeuArgAlaIleThr
                                                         TCACTTGCAGCCAAAATGGAAGAAATTAATGTTCCTTTGACTGTTGATTT
                                                                                                                                                              SerLeuAlaAlaLysIleGluGluThrGluValProMetLeuIleAspLe
                                                                                                                                                                                                                                                           euProSerGlyLysGlyTrpIleLeuGlnLeuLeuAlaValAlaCysLeu
                                                                                                                                                                                                                                                                                                  TTTTTGTTTGTCGATAAATTACTTGGATCGATTTCTATCTCTGTATGAAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /translation="MAADNIYDFVASNILCTETKSLCFDDVDSLTISQQNIETKSKDL SFNNGIRSEPLIDLPSLSEECLISFMVQREMEFLPKDDYVERLASGDLDLSVRKEALDW ILKAHMHYGFGELSFCISTINYLDFLSLYELFRSKTWTVQLAVAGLISAAKMEEIN PLTVDLQVGDDKFVFECKTIQRMELLVLSTLKWRMQAYTPYTFTDYFWRKMNGDQIPS RPLISGSMQLIUSIIRSIDFLEFRSSEIAASVAMSVSGEIQAKDIDKAMPCFFIHLDK GRVQKCYELIQDLTTATITTAAAASLVPQSPIGVLEAAACLSYKSGDERTVGSCTTSS
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71.554
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                      181
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2 others

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REFERENCE
AUTHORS
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AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                              Chenopodium rubrum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Caryophyllidae; Caryophyllales; Chenopodiaceae; Chenopodium.
1 (bases 1 to 1699)
                                                                                                                                                                                                                                  95447 Bayreuth, FRG
2 (bases 1 to 1699)
Renz,A., Fountain,M. and Beck,E.
Nucleotide sequence of a cDNA encoding a
photoautotrophic cell suspension culture
                                                                                                                                                                                                                                                                                                                     Pflanzenphysiologie,
os447 Bavreuth, FRG
                                                                                                                                                                                                                                                                                                                                                        Direct Submission
Submitted (18-DEC-1996) A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cycD1 gene;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 red goosefoot
                                                                                                                                                                                                                     Physiol. In press
                                                            /cell_type="photoautotrophic cells derived
tissue"
                                                                                                 /organism="Chenopodium rubrum"
/db_xref="taxon:3560"
/dev_stage="7 day old culture"
/clone_lib="lambda uniZAP-XR"
/gene="cycD1"
                                         /clone="pBluescript II
                                                                                                                                                                                                ocation/Qualifiers
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Universitaet Bayreuth, Universitaetsstr.
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of Chenopodium rubium
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                                                                                                                              CAATTGCTTGGGGTTGCTTGTTTATCTCTAGCTGCCAAGGTGGATGAAAC
                                                                                                                                                 GinLeuLeuAlaValAlaCysLeuSerLeuAlaAlaLysIleGluGhth 140
                                                                                                                                                                                                                                spArgPheLeuSerValHisAspLeuProSerGlyLysGlyTrpIleLeu 123
                                                                                                                                                                                                                                                                                        CCACTACAATTTTGGGCCACTTTGTGTTTATCTATCTGTAAACTACTTGG
                                                                                                                                                                                                                                                                                                            uValHisGlnPheGlyProLeuCysPheCysLeuAlaMetAsnTyrLeuA 107
                                                                                                                                                                                                                                                                                                                                                                  TTGGGT...GCTAGAAATCTGGTTATTGATTGGATTCATAAGGTTCAATC 746
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IsLeuProSerAspAspTyrIleLysArgLeuArgSerGlyAspLeuAsp
                                                                                     ATCGCTTCCTTTCGGCTTATGAATTACCT...GGCAAAGCTTGGATGATG
            heGluAlaLysSerValGlnArgMetGluLeuLeuValLeuAsnLysLeu
                                                   Ratio:
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[RNFDDFTLILLIIKEHNFEALISGFFVANHECLASLFDNREQHFLGLDYLKRFRNG
LDLGGARNLVLDWIHKYQSHYNRFGPLCYYLSVNYLDRFLSAYELPGKAWMQLLGVAC
LSLAAKVDETDVPLILDLQVSESKFVFEAKTIORMELLVLSTLKWRNGSYTPFSFIDY
FLYKLSGDKMFSKSLFQAIQLILSTIKGIDLMEFRPSEIAAAVAISVTQQTQIVEFT
DKAFSFLTDHVEKERLMKCVEIMHDLRMSSRSNGALASTSVPQSPIGVLDASACLSYK
SDDTSTPPSGSCGNSAISSPASAPPKRKKLDRTSQIS"
SDDTSTPPSGSCGNSAISSPASAPPKRKKLDRTSQIS"
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71.176
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/product="cyclin-D like protein"
/protein_id="cAA71244.1"
/db_xref="GI_1770190"
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                                                                                                                                                                                                                                                               Direct Submission
Direct Submission
Submitted (08-DEC-1994) J.A.H. Murray, Inst. of Biotechn.,Univ.
Cambridge, Tennis Court Road, Cambridge, CB2 1QT, UK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Soni,R., Carmichael,J.P., Shah,Z.H. and Murray,J.A. A family of cyclin D homologs from plants differentially by growth regulators and containing the conserved retinob protein interaction motif
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATCD2 1650 bp mRNA PLN A.thaliana mRNA for cyclin delta-2 (CycD2).
                                                                                               Submitted (07-JUN-1996)
Cambridge, Tennis Court
                                                                                                                                                                                                                                      Revised by [3]
3 (bases 1 to 1650)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Spermatophyta; Magnoliophyta; Spermatophyta; Tracheophyta; Spermatophyta; Spermatophyta; Spermatophyta; Embryophyta; Tracheophyta; Spermatophyta; Spermatophyta; Embryophyta; Tracheophyta; Spermatophyta; Embryophyta; Tracheophyta; Spermatophyta; Tracheophyta; Spermatophyta; Embryophyta; Tracheophyta; Spermatophyta; Tracheophyta; Spermatophyta; Tracheophyta; Spermatophyta; Spermatoph
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                               revised by [4]
4 (bases 1 to 1650)
                                                                                                                                                                                                                                                                                                                                                                                                         Murray, J.A.H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Plant Cell 7 (1), 85-103 (1995)
                                                                                                                                                               Direct Submission
                                                                                                                                                                                                   Murray, J.A.H.
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                                                                                                                                                                                                                                                                                                                                                                                                                                             (bases 1 to 1650)
                                                                                                   J.A.H. Murray, Inst.
Road, Cambridge, CB2
                                                                                                   of Biotechn.,Univ. 1QT, UK
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alignment_block:
US-09-530-209A-2 x ATCD2
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                      nSerGlu...
AGTTTTGCCCTGGAACTGATTATGTTAAGAGATTGCTTTCTGGTGATTTG
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Submitted (19-MAR-1998) J.A.H. Murray, Inst. of Biotechn., Cambridge, Tennis Court Road, Cambridge, CB2 lQT, UK
On Mar 28, 1998 this sequence version replaced gi:1402895.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Quality:
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/note="cyclin box"
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/db_xref="SMISS-PROT: P42752"
/translation="maenlacgetseswiidnddddinygggftneidynhqlfakdd
/translation="maenlacgetseswiidndddinygggftneidynhqlfakdd
/translation="maenlacgetseswiidneddinygggftneidlsynnoldlsungdlakgetd
wffggngsiphmgsssssslsserikemlyreiefepgftyvkrlaysclshaskmeetd
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wfitwcahythefhlciclsmyldreitsyelpwrlayldaltprefideydkisghyse
nliyrssrfilntkaiefldfrpseiaaaavsvsisgetecideekalssliyvkq
ervkrclnlmrsltgeenvrgtslsgegarvavravpaspvgvleatclsyrseertv
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66.111
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/protein_id="CAA58286.1"
/db_xref="GI:2995132"
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/tissue_type="whole seedlings"
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/db_xref="taxon:3702"
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DEFINITION ACCESSION
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LOCUS A85077
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Zea mays
                           A85077.1 GI:6733818
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                                          613 GCCGTCAGGAAGGACGCCATCGATTGGATTTGGAAGGTCATTGAGCATTA
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MUTRAY, J.A.

PLANTS WITH MODIFIED GROWTH

PATENT: WO 9842851-A 21 01-OCT-1998;

PATENT: WO 9842851-BENRY (GB); UN

MURRAY JAMES AUGUSTUS HENRY (GB); UN

LOCATION/QUALIFIERS

1. .1846
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Lin,X., Kaul,S., Rounsley,S.D., Shea,T.P., Benito,M.-I., Town,C.D.
Fujii,C.Y., Mason,T.M., Bowman,C.L., Barnstead,M.E.,
Feldblyum,T.V., Buell,C.R., Ketchum,K.A., Lee,J.J., Ronning,C.M.,
Koo,H., Moffat,K.S., Cronin,L.A., Shen,M., Vanaken,S.E., Umayam,L.
Tallon,L.J., Gill,J.E., Adams,M.D., Carrera,A.J., Creasy,T.H.,
Goodman,H.M., Somerville,C.R., Copenhaver,G.P., Preuss,D.,
                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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AC006592 AE002093
AC006592.5 GI:6598614
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Direct Submission
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127 of 255 of the
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Submitted (09-MAR-2000) The Institute for Genomic Research, 9712 Medical Center Dr., Rockville, MD 20850, USA on Dec 17, 1999 this sequence version replaced gi:4544435. The sequence and annotation of chromosome 2 were merged from those of the individual clones on this chromosome after removing overlaps. For detailed information, please see the TIGR web site (http://www.tigr.org/tdb/at/at.html).
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COMMENT

JOURNAL

Genes were identified by a combination of three methods: Gene prediction programs including GRAIL (ftp://arthur.epm.ornl.gov/pub/xgrail), Genefinder (Phil Green, University of Washington), Genscan (Chris Burge, http://gnomic.stanford.edu/GENSCANW.html), and NetPlantGene (http://www.cbs.dtu.dk/services/NetGene2/), searches of the complete sequence against a peptide database and plant EST databases at TIGR, and manual curations based on those analyses. Annotated genes are named to indicate the level of evidence for their annotation. Genes with similarity to other proteins are named after the database hits. Genes without significant peptide similarity but with EST similarity are named as 'unknown' proteins. Genes without protein or EST similarity, that are predicted by two annotated as 'hypothetical' proteins. Genes encoding tRNAs are predicted by tRNAscan-SE (Sean Edy), http://genome.wustl.edu/eddy/tRNAscan-SE/). Simple repeats were identified by repeatmasker (Arian Smit, http://ftp.genome.washington.edu/RM/RepeatMasker.html). Genes are numbered from the top to bottom of the chromosome.

We thank the CSHL/WashU/ABI consortium for sequencing BAC clones F6P23, F5J6, 717A5, and T13L16, the ESSA group for sequencing clone F13D4, and Scott Jackson, Jiming Jiang, Klaus Meyer, Eric Richards and Satoshi Tabata for helpful assistance. In addition, we would like to thank the TIGR Bioinformatics Department, especially Lixin Zhou, Hanif Khalak, Michael E. Heaney, Lily Fu, Feng Liang, Jeremy Peterson, Michael Holmes, and Delwood Richardson for software and database support.

This work was supported by the National Science Foundation Department of Energy and the US Department of Agriculture.

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FEATURES
mRNA
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gene
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="hypothetical protein"
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alignment_block:
US-09-530-209A-2 x AC006592/rev
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Ratio: 2.047
Percent Similarity: 43.058
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68164 TCAAATCTGGTTTGGTCTCTTTTTGTGCTTTGTGATTGAGTTTAAGTGTG 68115
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                                                                                                                                                                                                 AspLeuAsnValGlyArgArgAspAlaLeuAsnTrpIleTrpLysAlaCy 89
                                                                                                                                                                                                                                         AGTTTTGCCCTGGAACTGATTATGTTAAGAGATTGCTTTCTGGTGATTTG
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                                                                                                                                                                                                                                                                sGluVal.....
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Gaps: 19
Identity: 28.120
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91		
68114	TTCTTTGATCAGTTTGATAGCTCATTCATTCTCTGATGTATTTATT	
68064	ATTAATTGAATCTTCTCTATAGATTGAGGTATTGATCTTGTTGAGTAATT	68015
92	. E	92
68014	TTGTCTTTAATGCCAATTGTTCTACAGGTTTGTGCTCATTAC	67965
93 67964	GlnPheGlyProLeuCysPheCysLeuAlaMetAsnTyrLeuAspArgPh::::	109 67915
109	LeuSerValHisAspLeuPro	116
67914	TAAGTTGCATCGTCTTTGCGGATTGGT	67865
116		116
67864)GAGACAATACGATGACCGGTTTGTGTGTTTTCGATTGC	67815
117 67814	SerGlyLysGly.TrpIleLeuGlnLeuLeuAlaValAlaCysLeuS :::	132 67765
132 67764	ysIleGluGluThrGluValProMetLeuIleAspLeu ::: AAATGGAAGAAACTGATGTCCTCACATTGTTGATTTA	148 ; 67715
148		148
67714	atttagtccttaatagcttcagtcttcttacgaaga	67665
67664	AATCGAGGTTTTAGTGGAACTAATCTTGAAATGTTGTTCCTAT	67615
149 67614	GlnValGlyAspProGlnPheValPheGluAlaLysSerValGlnArg ::::	164 67565
165 67564	MetGluLeuLeuValLeuAsnLysLeuLysTrpArgLeuArgAlaIleTh ::: ::: ::: arggagcTTTTGGTTGTCACCACTTTGAATTGGAGATTGCAAGCTCTAAC	181 ·
181 67514	rProCysSerTyrIleArgTyrPheLeuArgLysMetSerLysCysAspG 	198 _. 67474
198 67473	InGluProSerAsnThrLeuIleSerArgSerLeuGinValIleAlaSer:::	214 67424
215 67423	ThrThrLysGly	218 67374
218	:	218
67373	CTTTCTTTATTTGCAACTAACTTGGCTTTGTTTAATGAGGAAGGCTGATA	67324
219 67323	IleAspPheLeuGluPheArg	225 67274
226 67273	ProSerGluAlaAlaAlaAlaValAlaLeuSerValSerGlyGl 	240 67224
240	n Leng I n	343

CDS .	TITLE TITLE JOURNAL COMMENT FEATURES SOURCE	JOURNAL MEDLINE REFERENCE AUTHORS TITLE JOURNAL REMARK REFERENCE AFFRENCE	SOURCE ORGANISM ORGANISM REFERENCE AUTHORS TITLE	seq_name: g seq_documen LOCUS DEFINITION ACCESSION VERSION KEYNORDS	Ω — e	294 r) 66929 C	281 . . 66973 G	273 . 67023 To	262 gV 67073 GC	255 67123 TT	243 67173 AA	67223 AJ
/originism Figuropsis tratique /variety="coctype Landsberg erecta" /db_xref="taxon:3702" /dev_stage="seedlings, stage 2 leaves" /tissue_type="whole seedlings" /clone_lib="pfL61" 1041111 /codon_start=1	Direct Submitted Submitted Cambridge On Mar 28	Plant Cell 7 (1), 85-103 (1995) 95210930 2 (bases 1 to 1951) 2 (bases 1 to 1951) Murray, J.A.H. Direct Submission Submitted (O8-DEC-1994) J.A.H. Murray, Inst. of Biotechn., Univ. of Cambridge, Tennis Court Road, Cambridge, CB2 1QT, UK revised by [3] 3 (bases 1 to 1951) Murray, J.A.H.	thale cress. Arabidopsis thaliana Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis. 1 (bases 1 to 1951) Soni,R., Carmichael,J.P., Shah,Z.H. and Murray,J.A. A family of cyclin D homologs from plants differentially controlled by growth regulators and containing the conserved retinoblastoma	<pre>gb_pl:ATCD1 intation_block: ATCD1</pre>	erSer 303	rPheLys	ThrProAsnGlyValLeuGluValSerAlaCysCysPheSe 294 :::	AspGlySerAspLeuCysSerGln	gValLysLysIleGlyGluMetIleGluSer	PheSerLeuLeuGlnLysGluAr 262	ArgValHisPheAspAsnSerSerPheSerProLeu 254 ::::::::: ::::::::::::	::: AACAGAATGCATTGATGAGGAAAAGGCACTGTCTAGTCTCATATATGTAA 67174

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BASE COUNT
ORIGIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    lnSerGluSerGlu...........GluIleIleMetGluMetValGlu 52
                                                                                                                                                                                 ysIleGluGluThrGluValProMetLeuIleAspLeuGlnValGlyAsp
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                                                                                                                                                                                                                                                                                                               sGlyTrpIleLeuGlnLeuLeuAlaValAlaCysLeuSerLeuAlaAlaL 136
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TCGATCTCCGATGCTTCC...GCTAGAGAAGATTCCGTCGCATGGATTC 371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LysGluLysGlnHisLeuProSerAspAspTyrIleLysArgLeuArgSe 69
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AGATGGAGGAAATTCTCGTTCCTTCTTTTTGATTTTCAGGTTGCAGGA 571
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1019..1051
/note="pest motif, p
a 327 c ~ 451 g
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IKEASFLEYWPSSIAAAILCVANELPSLSSTLTRPSDESSSPCKRRKLSGYSWVGDETSTS
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VERSION
KEYWORDS
SOURCE
ORGANISM
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AUTHORS
TITLE
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alignment_block:
US-09-530-209A-2 x A85060
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                                                                                                                                                    ORIGIN
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                                                                                                                                                                  BASE COUNT
                                                                                                                                                                                                                                   FEATURES
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Percent Similarity:
                                                                                                                                                                                                                                                                     JOURNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          rThrLysGlyIleAspPheLeuGluPheArgProSerGluAlaAlaAlaA
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                                       luValSerAlaCysCysPheSerPheLysThrHisAspSerSerSerSer 303
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REFERENCE
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The expression of D-cyclin genes define distinct developmental zones in Antirrhinum apical meristems and is locally regulated
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Submitted (18-OCT-1999) Doonan J.H., Cell Biology, Jo
Centre, Colney Lane, Norwich, NR4 7UH, UNITED KINGDOM
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1 (bases 1 to 1162)
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KQPKVLPQLRVMTRASLASSESSSSTSSSPSYKRRKLNNSSRADDDKESSDYGV"
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ESIAGLLEDERDLAGVNSSSSNGSVDSSTRTESTAWILKVQRYGGPQPLTAYLAVSYF
DRFINAHHLPKLNGWPOLLSVACLSLAAKNEESLVPSLLDLQVEGANETEPRNIQF
MELLVLRVLDWRLRSISPFCYLSFFALKIDPTGTYTGFLTSRAKEIILSTVQETSLIE
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/protein_id="CAB61221.1"
/db_xref="GI:6448480"
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/db_xref="taxon:4151"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /gene="cycD1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /dev_stage="flower spike"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ocation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1162 bp
                  .. IleGluIleSerIleProGlnMetGlyPhe
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cyclin
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6
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                                                             223
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259

39

TGCCGGAATATACTTCCGACGTGGAA...TCTATTCCG......
SerGlnSerGluSerGluGluIleIleMetGluMetValGluLySGluLy

.....ACGGACGTCGATGAATCTATCGCCGGACTTTTAGAAGACGAGAG

258 55 302

55

303 AGAT.....CTCGCCGGAGTTAACTCTAGCTCCT

331

sGlnHisLeuProSerAspAspTyrIleLysArgLeuArgSerGlyAspL 72

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seq_documentation_block:
LOCUS ATCD3
                                                                                    seq_name: gb_pl:ATCD3
VERSION
              ACCESSION
                             DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 432
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     482
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           382 CTCAAGGTGCAACGTTATTACGGTTTTCAGCCGTTAACGGCGTATCTCGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        332 CTAATCAATCCGTTGATTCTTCTACTAGAACAGAATCTACCGCATGGATC
                                                                                                                                                                                                                                                                                                                                                                                                 215
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              582 AGCAAACTTTATTTTTGAACCAAGAATATCCAAAGAATGGAGCTTCTTG
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                                                                                                                                                                                                                                                                                                                                                                    767
                                                                                                                                                                                                                                                                                                                                                                                                                                717
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                                                                                                                                                                                                                                                                          248
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                                                                                                                      934 ATTCAAGGAGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CGTTAGCTACTTCGATCGTTTTCTAAACGCCCATCACTTGCCGAAGTTGA 481
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TrpLysAlaCysGluValHisGlnPheGlyProLeuCysPheCysLeuAl 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LysIleGluGluThrGluValProMetLeuIleAspLeuGlnValGlyAs 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     alleuAsnLysLeuLysTrpArgLeuArgAlaIleThrProCysSerTyr 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        pProGlnPheValPheGluAlaLysSerValGlnArgMetGluLeuLeuV 169
                                                                                                                                                                                                                                                                                                                                  AlaValAlaLeuSerValSerGlyGluLeuGlnArgValHisPheAspAs 248
                                                                                                                                                                                                                                                                                                                                                                    hrThrLysGlyIleAspPheLeuGluPheArgProSerGluAlaAlaAla 231
                                                                                                                                                                                                                                                                                                                                                                                                                                AACCTATACAGGTTTCCTGACGTCAAGGGCTAAAGAAATTÄTTCTCTCÄA 766
                                                                                                                                                                                                                                                                                                                                                                                                                                                          nThr.....LeuIleSerArgSerLeuGlnValIleAlaSerT 215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CTCAGCTTTTTCGCACTCAAAATC......GACCCAACTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IleArgTyrPheLeuArgLysMetSerLysCysAspGlnGluProSerAs 202
                                                                                                                                                                                                            ysIleGlyGluMetIleGluSerAspGlySerAspLeuCysSerGlnThr 281
                                                                                                                                                                                                                                                                     nSerSerPheSerProLeuPheSerLeuLeuGlnLysGluArgValLysL 265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TGCTTAGGGTTTTAGATTGGAGACTTCGGTCAATATCTCCATTTTGTTAT
                                                                                                                                                    ProAsnGlyVal 285
                                                                                                                                                                                 CATGGTGTGATGGACTTCACAAAGATAATATTGCTAGTTGCATCAAACTG 933
                                                                                                                                                                                                                                                                                                           GCAACAATGCTTTCATCGGCAAATGATCTG......
                                                                                                                                                                                                                                           .....CCAAAATTTTCTTTCATCACTGCTCAACATGCTGAGG
             A thaliana mRNA for X83371
X83371.1 GI:2995133
                                                                                                                         945
                                               1632 bp
                                cyclin delta-3
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REFERENCE
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SOURCE
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AUTHORS
TITLE .
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MEDLINE
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                                                                                                                                                                                                                                                                                                                                                                                    BASE COUNT
ORIGIN
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                                                                                                                                                                               alignment_block:
US-09-530-209A-2 x ATCD3
                                                                                                                                                                                                                                                                                              alignment_scores:
Quality:
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TITLE
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Percent Similarity:
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                                                                                                                                 Align seg 1/1 to: ATCD3
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                                        25
pGluThrPro.....IleGluIleSerIleProGlnMetGlyPheSerG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

1 (bases 1 to 1632)
Soni,R., Carmichael,J.P., Shah,Z.H. and Murray,J.A.
Soni,R., Carmichael,J.P., Shah,Z.H. and Murray,J.A.
A family of cyclin D homologs from plants differentially controlled by growth regulators and containing the conserved retinoblastoma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Direct Submission Submitted (08-DEC-1994) J.A.H. Murray, Inst. of Biotechn.,Univ. Cambridge, Tennis Court Road, Cambridge, CB2 1QT, UK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cyclin; cyclin delta-3. thale cress.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Direct Submission
Submitted (19-MAR-1998) J.A.H. Murray, Inst. of Biotechn.,Univ. Cambridge, Tennis Court Road, Cambridge, CB2 1QT, UK
On Mar 28, 1998 this sequence version replaced gi:603508.

Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            revised by [3]
3 (bases 1 to 1632)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Murray, J.A.H
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Plant Cell 7 (1), 85-103 (1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Murray,J.A.H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (bases 1 to 1632)
                                                                                                                                                                                                                                                                                                                                                                                                                 478
                                                                                                                                                                                                                                                                                                                                                                                                               /note="cyclin box"
1169. .1393
/note="pest motif, page 1369 c 317 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /product="Gyclin delta-3"
/product="Gyclin delta-3"
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SSSPTVVLOQDLFWEDDDLVTLFSKEEEGGLSCLDDVYLSTDRKEAVGWILKVNAHVG
ESTILANULAITYLDKFICSYSLORDKPWMLQLVSVACLSLAAKVEETGVPFLLLDFQVE
ESTILANULAITYLDKFICSYSLORDKFWMLQLVSVACLSLAAKVEETGVPFLIKCHR
ETMYVFEAKTIORMELLILSTLEWKMHLJTP:SSVDHIIRLGVLKNIKEEVKTCV
LLLSVISDSFTGYLDSVVAAATMMRIIGVDDFDPLSYQTMILGVLKNIKEEVKTCV
DLILOLPVDRICLGIOLOSSKKRKSHDSSSSLNSPSCYIDANPFNSDESSNDSWSASS
CNPPTSSSSPQQQPPLKKNRGAEENEKKRPILHLPWAIVATP"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="pes 521. .838
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /dev_stage="seedling, stage 2 leaves"
/tissue_type="whole seedlings"
/clone_lib="pFL61"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /variety="ecotype Landsberg erecta"
/db_xref="taxon:3702"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     organism="Arabidopsis thaliana"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  codon_start=1
                                                                                                                                                                                                                                                     398.00
2.041
60.559
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      'note="LxCxE motif"
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                                                                                                                                           from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           pest motif, potential"
                                                                                                                                                                                                                                                     Gaps:
Percent Identity:
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                                                                                                                                             1632
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468 t
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ORGANISM
                                                                                                                                                                                                                                                                     alignment_block:
US-09-530-209A-2 x AMA250397
                                                                                                                                                                                                                                                                                                                                                                                            alignment_scores:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BASE COUNT
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                                                                                                                                                                                                                                                                                                                                    Percent Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CDS
                                                                                                                                                        146 GCTCTGTACTGTGAGGAAGAACAAAACTGGGACAATGGTGAAATCATCAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      source
                                  42 luSerGluGluIleIle.....MetGluMetValGluLysGluLysGln 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CGATTCATCATCATCG
TGAAACATGATTTGTTATGTGGTGTAGATGATGATGATGATAAAGAA
                                                                            TGACTGTTTCATTGAAGAACAAGAACCC
                                                                                                                 pGluThrProIleGluIleSerIleProGlnMetGlyPheSerGlnSerG
                                                                                                                                                                                           {\tt SerLeuLeuCysThrGluSerAsnValAspAspGluGlyMetIleValAs}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaudin,V., Lunness,P., Fobert,P., Towers,M., Riou-Khamilchi,C., Murray,J., Coen,E. and Doonan,J.H.

The expression of D-cyclin genes define distinct developmental zones in Antirrhinum apical meristems and is locally regulated by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnollophyta; eudicotyledons; core eudicots; Asteridae; euasterids I; Lamiales; Veronicaceae; Antirhinum. 1 (bases 1 to 1140)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Direct Submission
Submitted (18-OCT-1999) Dooman
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 snapdragon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cycD3a gene; cyclin D3a.
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                                                                                                                                                                                                                                                                                                                                                                         Quality:
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                                                                                                                                                                                                                                                                                                                                                     Ratio:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /product="cyclin D3a"
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FSALTAVIAVNYLDRFLCTFCPGQDKFWMYQLAAVACLSLAKVEETGVPLLLDLQVE
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LLLSLTTDCRFWCHLPSALATATMLYVISSLEPCIGVEYQDQLINILGINKDKVEECC
LLLSLTTDCRFWCHLPSALATATMLYVISSLEPCIGVEYQDQLINILGINKDKVEECC
KLIQEVATSVHFQSGNKRKFGSLPYSPKGVVDISFSCDDSWPLDSTASVSSSPEHLSK
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	saspSerSerSerSerTyrThrHisLeuS	298 1066
298 1065	ProAsnGlyValLeuGluValSerAlaCysCysPhe	282 1016
281 1015	euCysSerGln	277 966
277 965	sGluArgValLysLysIleGlyGluMetIleGluSer ::::: ::::: GGACAAAGTGGAGGAATGTTGTAAGTTAATACAAGAA	260 916
260 915	ValHisPheAspAsnSerSerPheSerProLeuPheSerL ::::::::::::::::::::::::::::::::::	244 872
243 871	laAlaAlaValAlaLeuSerValSerGlyGluLeuGlnA ::: ::: :::: :::	230 822
230 821	hrLysGlyIleAspPheLeuGluPheArgProS ::: rTACCGATTGTAGATTCATGTGCCATCTTCCAT	213 772
213 771	SerAsnThrLeuIleSerArgSerLeuGl 	197 737
196 · 736	TyrPheLeuargLysMetSer	184 687
184 686	rgAlaIl :: ATCCAGT	167 637
167 636	GlyAspProGlnPheValPheGluAlaLysSerValGlnArgMetGluLe :::::::::: ::: :::::	151 587
150 586	3 - 4	134 537
134 536	eLeuGlnLeuLeuAlaValAlaCysLeuSerLeuA :	117 487
117 486	TyrLeuAspArgPheLeuSerValHisAspLeuProSe 	101 437
100 436	<pre>lHisGlnPheGlyProLeuCysPheCys ::::: :: cTaTTCTTTTTCTGCTCTCACTGCGGTT</pre>	84 387
84 386	LeuAspLeuAsnValGlyArgArgAspAlaLeuAsnT 	67 337
336	GTGTAAAGAGCAGGAATATGAACTGTACAGAGT	57 287

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/SIDS2/gcgdata/geneseq/geneseqn/Na199 DAT: AAZ19959 /SIDS2/gcgdata/geneseq/geneseqn/Na199 DAT: AAX19959 /SIDS2/gcgdata/geneseq/geneseqn/Na199 DAT: AAX19886 + /SIDS2/gcgdata/geneseq/geneseqn/Na199 DAT: AAX13886 + /SIDS2/gcgdata/geneseq/geneseqn/Na2000 DAT: AAX13888 + /SIDS2/gcgdata/geneseq/geneseqn/Na2000 DAT: AAX13888 + /SIDS2/gcgdata/geneseq/geneseqn/Na2000 DAT: AAX13723 + /SIDS2/gcgdata/geneseq/geneseqn/Na2000 DAT: AAX13723 + /SIDS2/gcgdata/geneseq/geneseqn/Na2000 DAT: AAX13723 + /SIDS2/gcgdata/geneseq/geneseqn/Na2000 DAT: AAX13956 + /SIDS2/gcgdata/geneseq/geneseqn/Na2000 DAT: AAX13956 + /SIDS2/gcgdata/geneseq/geneseqn/Na2000 DAT: AAX13968 + /SIDS2/gcgdata/geneseq/geneseqn/Na2000 DAT: AAX19688 + /SIDS2/gcgdata/geneseq/geneseqn/Na199 DAT: AAX19964 + /SIDS2/gcgdata/geneseq/geneseqn/Na199 DAT: AAX1964 + /SIDS2/gcgdata/geneseq/geneseqn/Na199 DAT: AAX19688 + /SIDS2/gcgdata/geneseq/geneseqn/Na199 DAT: AAX1988 + /SIDS2/gcgdata/geneseq/geneseqn/Na199 DAT: AAX16988 + /SIDS2/gcgdata/geneseq/geneseqn/Na199 DAT: AAX16989 + /SIDS2/gcgdata/geneseq/geneseqn/Na199 DAT: AAX03187 + /SIDS2/gcgdata/geneseq/geneseq/geneseqn/Na199
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/SIDS2/gcgdata/geneseq/geneseqn/NA2000.DAT:AAX3884 +
/SIDS2/gcgdata/geneseq/geneseqn/NA1998.DAT:AAV33889 +
/SIDS2/gcgdata/geneseq/geneseqn/NA2000.DAT:AAZ94581 +
/SIDS2/gcgdata/geneseq/geneseqn/NA2000.DAT:AAZ94582 +
/SIDS2/gcgdata/geneseq/geneseqn/NA2000.DAT:AAZ94583 +
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Database sequences: 930621
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-Q-/G9n2_1/USPTO_Spool/US9953029/runat_19012002_145800_20232/app_query.fasta_1.371
-DB=N_Geneseq_1101 -QFMT=fastap -SUFFIX=rng -GAPOP=12.000
-GAPEXT=4.000 -MINMATCH=0.100 -LOOPECL=0.000 -LOOPEXT=0.000
-GAPOP=4.500 -QFAPEXT=0.050 -YGAPOP-10.000 -YGAPEXT=0.500
-FGAPOP=6.000 -FGAPEXT=7.000 -YGAPOP=10.000 -YGAPEXT=0.500
-DELOP=6.000 -DELEXT=7.000 -YGAPOP=10.000 -YGAPEXT=0.500
-DELOP=6.000 -DELEXT=7.000 -START=1 -MATRIX=blosum62
-TRANS=human40.cdi -LIST=45 -DCCALIGN=200 -THR_SCORE=pct
-THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pfs
-NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USER=US09530209_@CGN1_1_284 -NCPU=6 -ICPU=3 -LONGLOG
-USER=US09530209_@CGN1_1_284 -NCPU=6 -ICPU=3 -LONGLOG
-USCR=US09530209_@CGN1_1_284 -NCPU=6 -ICPU=3 -LONGLOG
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                                                                                                    The DNA sequence, vectors containing it, protein encoded by it, or antibodies recognising the protein can be used for modulating plant cell cycle, plant cell division and/or growth, for influencing the activity of mitogenic cyclin in a plant cell, as positive or negative regulator of cell proliferation, for modifying the growth inhibition caused by environmental stress conditions, or for use in a screening method for the identification of inhibitors or activators of cell cycle proteins. A compound which is an activator or inhibitor of the mitogenic cyclin can be used as a growth regulator and/or herbicide. The proteins can also be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   growth regulator; herbicide; cell division progression; ds
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                                                                                                                                                                                                                                                                                                                            This sequence encodes the mitogenic cyclin, CYCD4, of the invention. The DNA sequence, vectors containing it, protein encoded by it, or
                                                                                                                                                                                                                                                                                                                                                                                                               Claim 1; Page 47-49; 57pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DNA sequence encoding a mitogenic cyclin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Arabidopsis thaliana.
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Sequence 927 BP; 269 A;
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                                                                             used to influence cell division progression in yeast, mammals and
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proliferation;
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D-type cyclin; growth; plant; cell-division control; phosphorylation; CDC; Rb; retinoblastoma; germination; flowering; seed; fruit; root development; ds.
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                                                                                 This sequence represents the CYCD2;1 cDNA from Nicotiana tabacum which encodes a D-type cyclin. The sequence can be used to alter the growth encodes a D-type cyclin. The sequence can be used to alter the growth characteristics or architecture of plants by altering the (functional) characteristics or architecture of plants by altering the (functional) level in the plant cells of a cell-division controlling protein that can level in the plant cells of a cell-division controlling protein that can be composed by the protein of the cyclin gene is used to increase or decrease the growth modulation of the cyclin gene is used to increase not decrease the rate, provide faster germination, reduce time to flowering, increase the raduce height and to delay flowering in a range of plants, e.g. legumes, grasses, maize, oliseed rape, wheat, tomato, rice, barley, sunflower, caracteristics and controlled the cyclin 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO9842851-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nicotiana tabacum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Regulating growth and structure of plants by modulating protein that controls cell division - specifically a D-type cyclin, and related chimeric genes and transformed cells and plants, used to alter growth rate, flowering, seed production etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-OCT-1998.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 1998-532012/45.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Murray JAH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (UYCA-) UNIV CAMBRIDGE TECH SERVICES LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   26-MAR-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 24-MAR-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 14; p52-53; 75pp; English.
Sequence 1284 BP; 415 A;
                                                                carnation, chrysanthemum,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          97EP-0302096
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       98WO-EP01701
                179 C;
                                                                          rose,
                261 G; 429 T; 0 other;
                                                                              tulip, etc.
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alignment_scores:
                                                                                                                                                             alignment_block:
                                                                                                                                  Align seg 1/1 to:
                                                                                                                                                     US-09-530-209A-2 x AAV33884
                                                                                                                                                                                 Percent Similarity:
                                                       232 AGAAACAAAAAGTCTTTGTTTTGATGATGTTGATTCTTTGACTATAAGTC
                                                                                              182
                 282
                                                                          u
u
                                    26
41
                                                                                            rGluSerAsnVal.....
                  luThrProIleGluIleSerIleProGlnMetGlyPheSerGln.....
                                                                                                                                                                                                   Quality:
                                                                                                                                                                                           Ratio:
                                                                                                                                      AAV33884
                                                                                                                                                                                  722.50
2.961
71.554
                                                                                                                                      from:
                                                                                                                                                                                 Length: 341
Gaps: 10
Percent Identity: 48.094
                                                                           .AspAspGluGlyMetIleValAspG 26
                                                                                                                                      ب
  .SerGluSerGluGluIleIleMe
                                                                                                                                      to: 1284
                                             40
                                                              281
                                                                                                    231
       48
                         331
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root development;

ds

Maize CYCD2

25-JAN-1999

(first entry)

D-type cyclin; growth; plant; cell-division control; phosphorylation; CDC; Rb; retinoblastoma; germination; flowering; seed; fruit;

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1070
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                                                                                                                                                                                                                                                       ysLysIleGlyGluMetIleGlu.....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AATCCCATCTCGGCCGTTGATTTCTGGATCAATGCAACTGATATTAAGCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          euProSerGlyLysGlyTrpIleLeuGlnLeuLeuAlaValAlaCysLeu 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LeuAsnTrpIleTrpLysAlaCysGluValHisGlnPheGlyProLeuCy
                   ....SerSerSerSerTyrThr 305
                                                                                                                                                                                   SerAspGlySerAspLeuCysSerGlnThrProAsnGlyValLeuGluVa 288
                                                                                                                                                                                                                          AGAAGTGTGTTGAACTGATTCAAGATTTGACAACTGCTACTATTACTACT
                                                                                                                                                                                                                                                                                                                                   nSerSerPheSerProLeuPheSerLeu...LeuGlnLysGluArgValL 264
                                                                                                                                                                                                                                                                                                                                                                          TCAGTGGCAATGTCTGTTTCAGGGGAAATACAAGCAAAAGACATTGATAA
                                                                                                                                                                                                                                                                                                                                                                                                           AlaValAlaLeuSerValSerGlyGluLeuGlnArgValHisPheAspAs 248
                                                                                                                                                                                                                                                                                                                                                                                                                                                  TAATAAGAAGTATTGATTTCTTGGAATTCAGGTCTTCTGAAATTGCAGCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   nGluProSerAsnThrLeuIleSerArgSerLeuGlnValIleAlaSerT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CCTTACACATTCATAGATTATTTATGAGAAAGATGAATGGT...GATCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TGCCAAGAAGTAAAACTTGGACAGTGCAATTGTTAGCTGTGGCCTGTCTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TTTTTGTTGTCGATAAATTACTTGGATCGATTTCTATCTCTGTATGAAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CTTGATTGGATTTTGAAGGCTCATATGCACTATGGATTTTGGAGAGCTGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AGAGATTGAGAAGTGGAGATTTGGATTTGAGTGTG...AGAAAAGAGGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ysArgLeuArgSerGlyAspLeuAspLeuAsnValGlyArgArgAspAla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TTTTATGGTGCAAAGGGAAATGGAGTTTTTGCCTAAAGATGATTATGTCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  tGluMetValGluLysGluLysGlnHisLeuProSerAspAspTyrIleL
CATGTACAACTTCTTCACATACT
                                                                                                           lSerAlaCysCysPheSerPheLysThrHisAsp......
                                                                                                                                                GCTGCTGCTGCCTCATTAGTACCTCAAAGTCCTATTGGAGTGTTGGAA..
                                                                                                                                                                                                                                                                                                GGCA....ATGCCTTGCTTCATACACTTAGACAAGGGTAGAGTGC 1019
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ProCysSerTyrIleArgTyrPheLeuArgLysMetSerLysCysAspGl 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           uGlnValGlyAspProGlnPheValPheGluAlaLysSerValGlnArgM
                                                                    .GCAGCAGCATGCTTGAGCTACAAAAGTGGTGATGAGAGAACAGTTGGAT 1166
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This sequence represents the CYCD1:1 cDNA from Zea mays which encodes a D-type cyclin. The sequence can be used to alter the growth characteristics or architecture of plants by altering the (functional) level in the plant cells of a cell-division controlling protein that can bind to, or phosphorylate, an Rb-like protein, such as a D-type cyclin. Modulation of the cyclin gene is used to increase or decrease the growth rate, provide faster germination, reduce time to flowering, increase the number of flowers, sedds or fruits per plant, increase root development, reduce height and to delay flowering in a range of plants, e.g. legumes, grasses, maize, oilseed rape, wheat, tomato, rice, barley, sunflower,

growth rate, flowering,

WPI; 1998-532012/45.

Claim 14; p64-65; 75pp; English.

Regulating growth and structure of plants by modulating protein that controls cell division - specifically a D-type cyclin, and related chimeric genes and transformed cells and plants, used to alter

seed production etc.

PF PA XX

(UYCA-) UNIV CAMBRIDGE TECH SERVICES

CTD

97EP-0302096 98WO-EP01701

24-MAR-1998; 01-OCT-1998 W09842851-A1 Zea mays.

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alignment_block:
US-09-530-209A-2 x AAV33889
                                                                                                                                                                                                                                                                                                               SXCCCCCCCCCXXXTTTXXX
                                                                                                                                                                                                                                                                            alignment_scores:
                                                                                                                                                                                                                                          Ratio:
Percent Similarity:
                                                                                                                                                                                  Align seg 1/1 to: AAV33889
                                                                                                                                                                                                                                                                                                             Sequence 1846 BP;
                                                                                                                                                                                                                                                                                                                                   carnation, chrysanthemum, rose, tulip, etc.
                    28 ProIleGluIleSerIleProGlnMetGlyPheSerGlnSerGluSerGl 44
                                                                                                                                                          10 LeuLeuCysThrGluSerAsn......ValAspAspGluGl
                                           CCGCCGCCGCCACCGGGGTCGCCGTCGATGGGATTTTGACGGAGTTC
                                                                                        GGAGGAGTCCTCCTGGGCGGCCGCCGCCTACGCCGCCACGTGACACCGTCG
                                                                                                                                      CTGCTGTGCGCGGAGGACAACGCTGCTATTCTCGGCCTGGACGACGATGG
                                                             .....IleValAspGluThr
                                                                                                                                                                                                                                                                 Quality:
                                                                                                                                                                                                                                          621.50
2.762
63.202
                                                                                                                                                                                                                                                                                                             448 A; 425 C; 514 G; 458 T; 1 other;
                                                                                                                                                                                   from:
                                                                                                                                                                                                                                     Length: 356
Gaps: 10
Percent Identity: 39.888
                                                                                                                                                                                  to: 1846
... CTCTCGGA
                                            498
                                                                   27
                                                                                         448
                                                                                                               22
                                                                                                                                      398
                                                                                                                                                            21
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seq_documentation_block:
ID AAV33889 standard;
XX

CDNA ç

mRNA; 1846

/SIDS2/gcgdata/geneseq/geneseqn/NA1998.DAT:AAV33889

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1304
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                                                                                                                                         280
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        spAspTyrIleLysArgLeu.....ArgSerGlyAspLeuAspLeuAsn 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TGACTGCGTTGCGACGCTCGTGGAGAAGGAGGTGGAGCACATGCCCGCGG 562
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              uGluIleIleMetGluMetValGluLysGluLysGlnHisLeuProSerA 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           | ProMetLeuIleAspLeuGlnValGlyAspProGlnPheValPheGluA 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TTGGCAGTGGCTTGCTTTTGGCTTCGAAAATCGAAGAGACTTTTGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LeuAlaValAlaCysLeuSerLeuAlaAlaLysIleGluGluThrGluVa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TCCTCTCCACGTATGAGTTCCCTGAAGGCAGAGCTTGGATGACTCAGCTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             heLeuSerValHisAspLeuProSerGlyLysGlyTrpIleLeuGlnLeu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GCCGTCAGGAAGGACGCCATCGATTGGATTTGGAAGGTCATTGAGCATTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ValGlyArgArgAspAlaLeuAsnTrpIleTrpLysAlaCysGluValHi 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AGGGGTACCTCCAGAAGCTGCAGCGACGGCATGGGGACCTGGATTTGGCC
                                                                                                                                                                                                                                                                                                                   GAGTTCTGTAATTGAGAGAGCTGCTAGTAGCTGCAAATAT.....TTGG
                                                                                                                                                                                                                                                                                                                                                                                                                      ProSerGluAlaAlaAlaAlaValAlaLeuSerValSerGlyGluLeuGl
                                                                                                                                                                                                                                                                                                                                                                                                                                                           CGGACCTTGTCTTGAGCACCGCTAAAGGTGCTGAATTCGTGGTATTCAGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   laLysSerValGlnArgMetGluLeuLeuValLeuAsnLysLeuLysTrp 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       nArgValHisPheAspAsnSerSerPheSerProLeuPheSerLeuLeuG
                                                                                                                                                                                                                                                                                                                                                                                       CCCTCCGAGATTGCTGCCAGTGTTGCACTTGCTGCTATCGGCGAATGCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          euGlnValIleAlaSerThrThrLysGlyIleAspPheLeuGluPheArg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            sMetSerLysCysAspGlnGluProSerAsnThrLeuIleSerArgSerL 209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AGGATGCATGCTTACTGCTTGCTCATTTGTTGAATACTTTCTTCATAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ArgLeuArgAlaIleThrProCysSerTyrIleArgTyrPheLeuArgLy 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTGAGTGAT...CATGGTGCACCCTCCTTGCTTGCACGCTCTCGCTCTT
                                                                                                      ACAAAGCCCAATAGGTGTCCTGGACGCTGCAGCCTGTCTGAGTCAACAAA 130
                                                                                                                                                                           GCGGGAAGCATTGTCCTAAAGTCTGCTGGATCATCAATCTCCTCTGTGCC 125
                                                                                                                                                                                                                                               ACAAGGAGAGGGTTTTAAGATGCCATGAAATGATTCAAGAGAAGATTACT 120
HisAspSerSerSerSer 303
                                    GCGATGACGCTACTGTCGGGTCTCCTGCAGTATGTTAC
                                                                                                                                                                                                                                                                            lnLysGluArgValLysLysIleGlyGluMetIleGlu.....
                                                                                                                                        .GlnThrProAsnGlyValLeuGluValSerAlaCys.....
                                                                                                                                                                                                            .....SerAspGlySerAspLeuCysSer.....
                                                                  .....CysPheSerPheLysThr 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  142
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                                            1341
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AZ94581 standard; Db XX
AC AAZ94581;
AC AZ94581;
AZ94581;
AC AZ94581;
AC AZ94581;
AC AZ94581;
AC AZ94581;
AC AZ9458
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Maize cyclin D ZmCycD gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (PION-) PIONEER HI-BRED INT INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /SIDS2/gcgdata/geneseq/geneseqn/NA2000.DAT:AAZ94581
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
275..1351
/*tag= a
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; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CycD; cell division; cell cycle
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         McElver JA;
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Claim 1; Page 115-117; 134pp; English. Novel polynucleotides encoding maize cyclin D isoforms 1, 2 and 3, related proteins and antisense RNA useful for control of cell cycle ${\sf related}$

WPI; 2000-283589/24 P-PSDB; AAY79321.

CC gene that encodes cyclin D (CycD, see AAY79321), a protein necessary CC gene that encodes cyclin D (CycD, see AAY79321), a protein necessary CC cpt gene that encodes cyclin D (CycD, see AAY79321), a protein binds to CC cDK4, and the active CycD-CDK4 hyperphosphorylates retinoblastoma CC cDK4, and the active CycD-CDK4 hyperphosphorylates retinoblastoma CC associated protein, releasing the E2F transcription factor which CC cativates DNA synthesis. The invention provides maize CycD cycle regulation. Also provided are that are involved in cell cycle regulation. Also provided are cycle recombinant expression cassettes (including ZmCycD in sense or cycle are involved in cell cycle regulation. Also provided are recombinant expression, host cells, transgenic plants (especially CC corn, sorghum, sunflower, safflower, wheat, rice, alfalfa or coilseed Brassica) and antibody compositions. A claimed method of CC modulating the level of CycD protein in a cell comprises CC dividing the cell with a recombinant expression cassette comprising a CycD polynucleotide linked to a promoter, and cycD protein in the cell. The CycD protein is present in an amount CycD protein in the cell. The CycD protein is present in an amount CycD protein to alter cell division, increase the number of cells sufficient to alter cell growth, protein salter plant cycle protein, stalk, pollen, stamen) growth, produce organ ablation, cother cells are arreated in Cl or Go Dhase or in a particular cell chart cell are arreated in Cl or Go Dhase or in a particular cell that cells are arrested in GI or GO phase or in a particular cell cycle, improve response to environmental stress including dehydration, heat or cold, increase the number of pods per plant, increase the number of seeds per pod or ear, alter the lag time in seed development, provide hormone-independent cell growth, or development, provide hormone-independent cell

CATAGTTCTTCCACAAGC 1359

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US-09-530-209A-2 x AAZ94581
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Percent Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                increase the growth rate of cells in bioreactors. The level of CycD protein in the cells is transiently modulated by introducing CycD RNA or CycD polypeptides. CycD polynucleotides can be used to identify CycD interacting proteins. All claimed.
                                                                                                                                                                                                                                                      722
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                                                                                                                                                                                                                                                                                                                                           heLeuSerValHisAspLeuProSerGlyLysGlyTrpIleLeuGlnLeu 125
                                                                                                                                                                                                                                                                                                                                                                                                                                           spAspTyrIleLysArgLeu.....ArgSerGlyAspLeuAspLeuAsn 75
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                             sMetSerLysCysAspGlnGluProSerAsnThrLeuIleSerArgSerL
                                                            AGGATGCATGCTGCTTACTGCTTGCTTGAATACTTTCTTCATAA
                                                                             ArgLeuArgAlaIleThrProCysSerTyrIleArgTyrPheLeuArgLy
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ATTGAGTGAT...CATGGTGCACCCTCCTTGCTTGCACGCTCTCGCTCTT
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ID AAZ94582 standard;
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                                                                                                                                 WPI; 2000-283589/24.
P-PSDB; AAY79322.
                                                                                                                                                                                                                                                                                                                                                                                                      Maize; cyclin D; ZmCycD gene; CycD; cell division; cell cycle; transgenic plant; ss.
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                                        Claim 1; Page 120-121; 134pp; English.
                                                                      Novel polynucleotides encoding maize cyclin D isoforms 1, 2 and 3, related proteins and antisense RNA useful for control of cell cycle regulation \,
                                                                                                                                                                           Lowe KS, Tav
Hoerster GJ;
                                                                                                                                                                                                                                                     23-SEP-1998;
                                                                                                                                                                                                                                                                                 21-SEP-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                Maize cyclin D ZmCycD gene
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The present sequence is that of an isoform of the maize ZmCycD gene that encodes cyclin D (CycD, see AAY79322), a protein necessity.

necessary

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alignment_block: US-09-530-209A-2 \times AAZ94582
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                                                                                                                  248 AGGGGTACCTCCAGAAGCTGCAGCGACGGCATGGGGACCTGGATTTGGTC 297
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76 ValGlyArgArgAspAlaLeuAsnTrpIleTrpLysAlaCysGluValHi 92 ::: ||||:::|||||||::: ||| ::
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Percent Identity: 39.888
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298 GCCGTCAGGAAGGACCCCATCGATTGGAAGGTCATTGAAGCATTA 347 92 SGInPheGlyProLeuCysPheCysLeuAlaketAsnTylleuAspArpp 109 92 SGInPheGlyProLeuCysPheCysLeuAlaketAsnTylleuAspArpp 109 93 GCCGTCGCACGTTTGACTGCCGTTTTTGTCTGTGAAGCATAGAT 397 109 heLeuSerValHisAspLeuProSerGlyLysGlyTrpLleLeuGlnLeu 125 109 hCCCCCGCGTTGAACTGCCCGTTTTTGTCTGGAACTACCTCCACATAGAT 397 109 hCCCCCGCGTTGAATTGCTCCTGAAAGCAGAAGCATTGGATCAGCTC 447 126 LeuAlaValAlaCysLeuSerLeuAlaAlaLySILeGluGluThrGluVa 142 111	seq_seq_ ID XXX AC AC DT			
GCCGTCAGGAAGGACCCATCGATTGGATTGGAAGGTCATTGACATTA 347 SGInPheGlyProLeuCysPheCysLeuAlaMetAsnTyTLeuAspArgp 109 SGInPheGlyProLeuCysPheCysLeuAlaMetAsnTyTLeuAspArgp 109 CARTTTCGCACCGTTGATTGATTGTCTTGATACTCATAGAT 377 CARTTTCGCACCGTTGATTGACTTCCCTGAAGACCAACCTTGATACTCAGAT 397 CARTTTCGCACCGTTGATTGACTTCCCTGAAGACCAACCTTGAACTACCTCGATAGAT 11 LILLILLILLILLILLILLILLILLILLILLILLILLI	d n 1	3 8 8 7 3 5 9	4 4 2 9 0 4 4	2 4 4 4 9 9
	GCGATGACGCTACTGTCGGGTCTCCTGCAGTATGTTAC	AGTTCTGTAÄTTGÄGAGAGCTGCTAGTÄGCTGCAAATATTTGG 83 nLysGluArgValLysLysIleGlyGluMetIleGlu	LeuArgAlaIleThrProCysSerTyrIleArgTyrPheLeuArgLy 19:::::: :::	CAGGAAGGACGCCATCGATTGGATTTGGAAAGGTCATTGAGCATTA 34 heGlyProLeuCysPheCysLeuAlaMetAsnTyrLeuAspArgP 10 :::

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alignment_scores:
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                                                                                                                                                                                                                                                                                                         Sequence 1173 BP;
                                                                                                                                                                                                                                                                                                                                                                                      increase the growth rate of cells in bioreactors. The level of CycD protein in the cells is transiently modulated by introducing CycD RNA or CycD polypeptides. CycD polypucleotides can be used to identify CycD interacting proteins. All claimed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     increase the number of seems put pour cell growth, or seed development, provide hormone-independent cell growth, or the mrouth rate of cells in bioreactors. The level of
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seq_documentation_block:
This nucleotide sequence represents a portion of the cDNA insert conclone ceb5.pk0049.h5 encoding a portion (see AAY31897) of a corn cyclin delta-2 polypeptide. The clone was isolated from a corn cembryo (20 days after pollination) cDNA library. The invention cembryo (20 days after pollination) cDNA library. The invention cyclin delta-3 cyclin delta-2 and cyclin delta-3 cyclin delta-3 cyclin delta-2 and cyclin delta-3 cyclin delta-3 cyclin delta-3 cyclin delta-3 cyclin delta-3 cyclin delta-3 cyclin of a cyclin, in sense cyclineric genes encoding all or a portion of a cyclin, in sense cyclineric genes creatists in altered levels of the cyclin protein in a transformed cyclin set cell. This would have the effect of altering the regulation cyclin cyclin in those cells. The nucleic acid fragments may be cyclin a portion of cyclins in plant cells to enhance cell tissue cyclin plants, provide genetic tools to enhance cell cycle all or a portion of cyclins should facilitate studies of cell cycle in plants, provide genetic tools to enhance cell growth in tissue culture, increase the efficiency of gene transfer and help provide more stable transformations. The proteins can be used as targets cyclintate design and/or identification of inhibitors of those
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transgenic plant; herbicide;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New isolated plant cyclin genes, used to develop products for herbicides and for developing plant breeding programs -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (DUPO ) DU PONT DE NEMOURS & CO
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                                                                                                                                                                             240 GluLeuGlnArg......ValHisPheAs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    42 GluSerGluGluIleIleMetGluMetValGluLysGluLysGlnHisLe
                                                                                                                                                                                                                                                                                                                                         rArgSerLeuGlnValIleAlaSerThrThrLysGlyIleAspPheLeuG
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                                                                                                                                                                                                                                                                                                       GCAGTCCGCGGAGCTTATCTTGCGTGCGGCCAGAGGAACCGGCTGCGTCG
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                                                                                                                                                                                                                        GGTTCAGGCCGTCCGAGATCGCCGCCGCGGTTGCAGCCGCCGTGGCCGGA
                                                                                                                                                                                                                                             lupheArgProSerGluAlaAlaAlaAlaValAlaLeuSerValSerGly
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                                                     T.....AAGGAGCGGGTGT 110:
                                                                                                  pAsnSerSerPheSerProLeuPheSerLeuLeuGlnLysGluArgVal.
                                                                                                                                    GACGTGGACGACGCGGACGCGTCGAGAACGCCTGCTGCGCTCACGTAGA
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LysLysIleGlyGluMetIleGluSerAspGlySerAsp ::: |||||||| ::: |||
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AAC42423 standard; AAC42423; AAC42423; 17-OCT-2000 (firs AAC42423; 17-OCT-2000 (firs Arabidopsis thalia Hybridisation assa protein identifica metabolic pathway; Arabidopsis thalia EP1033405-A2. 06-SEP-2000; 2000E 25-FEB-1999; 99U 05-MAR-1999; 99U 07-MAR-1999; 99U 08-APR-1999; 99U 10-APR-1999; 99U 11-APR-1999; 99U 10-APR-1999; 99U 11-APR-1999; 99U 11-APR-1999; 99U 11-APR-1999; 99U 11-APR-1999; 99U 11-APR-1999; 99U 11-MAY-1999; 99U 12-MAY-1999; 99U 12-MAY-1999; 99U 13-MAY-1999; 99U 14-MAY-1999; 99U	1104 TGCGGTGCCAGGAAG 277 LeucysSer 1154 GACGCTACCGTGCCA 280GlnThrPr 180 CGTGCCGAGAGCCC 294 erPheLysThrHisA 11:11:11:11:11:11:11:11:11:11:11:11:11:
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PR 05 - NUG - 1999; 9918-0147260.
PR 08 - NUG - 1999; 9918-0147310.
PR 19 - NUG - 1999; 9918-0147415.
PR 11 - NUG - 1999; 9918-0147415.
PR 11 - NUG - 1999; 9918-014836.
PR 11 - NUG - 1999; 9918-014836.
PR 11 - NUG - 1999; 9918-014836.
PR 12 - NUG - 1999; 9918-014846.
PR 22 - NUG - 1999; 9918-014942.
PR 23 - NUG - 1999; 9918-014942.
PR 23 - NUG - 1999; 9918-014942.
PR 25 - NUG - 1999; 9918-014942.
PR 27 - NUG - 1999; 9918-014942.
PR 27 - NUG - 1999; 9918-014942.
PR 27 - NUG - 1999; 9918-014942.
PR 28 - NUG - 1999; 9918-014942.
PR 29 - NUG - 1999; 9918-014942.
PR 29 - NUG - 1999; 9918-01496.
PR 20 - NUG - 1999; 9918-01496.
PR 21 - NUG - 1999; 9918-015066.
PR 21 - NUG - 1999; 9918-015066.
PR 22 - NUG - 1999; 9918-0151080.
PR 23 - NUG - 1999; 9918-0151080.
PR 24 - SEEP - 1999; 9918-0151080.
PR 25 - SEEP - 1999; 9918-0151080.
PR 26 - SEEP - 1999; 9918-0151080.
PR 27 - SEEP - 1999; 9918-015263.
PR 28 - SEEP - 1999; 9918-015263.
PR 28 - SEEP - 1999; 9918-015263.
PR 29 - SEEP - 1999; 9918-015263.
PR 20 - CCT - 1999; 9918-015263.
PR 21 - CCT - 1999; 9918-015263.
PR 22 - CCT - 1999; 9918-015263.
PR 23 - CCT - 1999; 9918-015263.
PR 24 - CCT - 1999; 9918-015263.
PR 25 - CCT - 1999; 9918-015263.
PR 26 - CCT - 1999; 9918-015263.
PR 27 - CCT - 19
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alignment_scores:

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	CGCGAITCTCTGTGTAGCGAAACGAGITACCITCTCTALe erSerPheSerProLeuPheSerLeuLe	
24 89	laValAlaLeuSerValSerGlyGluLeuGlnArgValHisPheAspAsn 	232
85	rThrLysGlyIleAspPheLeuGluPheArgProSerGluAlaAlaAlaA : ::: ::: ::: :: CATAAAAGAAGCGAGCTTTCTTGAGTACTGGCCATCGAGTATAGCTGCAG	215 806
21! 80!	ThrLeuIleSerArgSerLeuGlnValIleAlaSerTh ::: ::::: :::::: ::: ACCTTTCTCGGGGTTCTTTATCTCCCATGCTACAGAGATTATACTCTCCAA	203 756
20; 75!	leArgTyrPheLeuArgLysMetSerLysCysAspGlnGluProSerAsn :::	186 721
186 720	LeuAsnLysLeuLysTrpArgLeuArgAlaIleThrProCysSerTyrI ::: ::::: 	169 671
169 670	ProGlnPheValPheGluAlaLysSerValGlnArgMetGluLeuLeuVa ::::::::: ::::::::	153 621
152 620	ysIleGluGluThrGluValProMetLeuIleAspLeuGlnValGlyAsp ::: -::: ::: AGATGGAGGAAATTCTCGTTCCTTCTCTTTTGATTTTCAGGTTGCAGGA	136 571
136 570	SGlyTrpIleLeuGlnLeuLeuAlaValAlaCysLeuSerLeuAlaAlaL: :::	
119 520	MetAsnTyrLeuAspArgPheLeuSerValHisAspLeuProSerGlyLy:::: ::: ::::	103 471
102 470	rpLysAlaCysGluValHisGlnPheGlyProLeuCysPheCysLeuAla ::: 	86 4 21
86 420	rGlyAspLeuAspLeuAsnValGlyArgArgAspAlaLeuAsnTrpIleT:::: ::: ::: ::::	69 374
69 373	LysGluLysGlnHisLeuProSerAspAspTyrIleLysArgLeuArgSe :::::	53 324
52 323	InSerGluSerGlu	40 274
40 273	eValAspGluThrProIleGluIleSerIleProGlnMetGlyPheSerG:	23 245
23 244	GluLeuSerLeuLeuCysThrGluSerAsnValAspAspGluGlyMetIl::::::: :::	7 207
	g 1/1 to: AAC42423 from: 1 to: 1337	Align se
	_block: 0-209A-2 x AAC42423	alignment US-09-53
	Quality: 443.50 Length: 316 Ratio: 2.092 Gaps: 11 Similarity: 67.089 Percent Identity: 37.025	Percent

Align seg 1/1

to: AAV33887

from: 1

to: 1788

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                                                                                                                                                          alignment_scores:
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                                                                          Percent Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                       This sequence represents the CYCD1;1 cDNA from Helianthus tuberosus which encodes a D-type cyclin. The sequence can be used to alter the growth characteristics or architecture of plants by altering the (functional) level in the plant cells of a cell-division controlling protein that can bind to, or phosphorylate, an Rb-like protein, such as a D-type cyclin. Modulation of the cyclin gene is used to increase or decrease the growth rate, provide faster germination, reduce time to flowering, increase the number of flowers, seeds or fruits per plant, increase root development, reduce height and to delay flowering in a range of plants, e.g. legumes, grasses, maize, oilseed rape, wheat, tomato, rice, barley, sunflower,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 14; p56-57; 75pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Regulating growth and structure of plants by modulating protein that controls cell division - specifically a D-type cyclin, and related chimeric genes and transformed cells and plants, used to alter growth rate, flowering, seed production etc.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         H.tuberosus CYCD1;1 gene
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                                                                                                                                                                                                                                                                                                                                 Sequence 1788
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175 pArgLeuArgAlaIleThrProCysSerTyrIleArgTyrPheLeuArgL
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                                           287 luValSerAlaCysCysPheSerPheLysThrHisAspSerSerSerSer
                                                                                                                                                                                                                                                                                            859 CAAGTGATCTTTCTAAATTCTCACTTATCAATGCTGATCATGCTGAATCA
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ATATTGCCGGTACATGTTCGAGT.....CATGACGGCTCGAGTGAG
                                                                                                ACAATCTCCAAA.
                                                                                                                                           eGluSerAspGlySerAspLeuCysSerGlnThrProAsnGlyValLeuG
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                                                                                                               CC DNA inserts in clones sahlc.pk003.17 and sr1.pk0001.95 encoding CC the entire soybean cyclin delta-1 protein (see AAV31894). These CC clones were respectively isolated from soybean sprayed with CAUCHOMER (MM) herbicide and soybean root cDNA libraries. The CC authority (TM) herbicide and soybean root cDNA libraries. The CC invention relates to isolated nucleic acid fragments (see AAX19953-66) CC encoding cyclin A, cyclin delta-1, cyclin delta-2 and cyclin delta-3 CC polypeptides (see AAX31889-902). It also relates to the construction CC of chimeric genes encoding all or a portion of a cyclin, in sense CC or antisense orientation, where expression of the chimeric gene CC results in altered levels of the cyclin protein in a transformed CC host cell. This would have the effect of altering the regulation CC collure growth. The availability of nucleic acid fragments may be CC culture growth. The availability of nucleic acid sequences encoding CC collure, increase the efficiency of gene transfer and help provide CC culture, increase the efficiency of gene transfer and help provide more stable transformations. The proteins can be used as targets CC enzymes that may be useful as herbicides.
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AAZ19958 standard; cDNA; 2259
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                                                                                      Sequence 2259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 7; Page 51-52; 68pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New isolated plant cyclin genes, used to develop products for use herbicides and for developing plant breeding programs - \,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAGAATCAGTTGGATGGATTCTCAAGGTACACGCGTACTATGGCTTTCAG
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                                                                                                        GlnArgValHisPheAspAsnSerSerPheSerProLeuPheSerLeuLe
                                                                                                                                                                                                                                                                               rLeuGlnValIleAlaSerThrThrLysGlyIleAspPheLeuGluPheA
                                                                                                                                                                                                                                                                                                                      TGCAAAGTAGATTCAACTGGAACTTTTATCCGGTTCCTTATTTCCAGGGC
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alignment_scores:
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ID AAZ19959 standard;
                                                                                                                                                                               CC clone se6,pk0028.fll encoding a portion of the cDNA insert in CC clone se6,pk0028.fll encoding a portion (see AAV31895) of a soybean CC cyclin delta-1 protein. The clone was isolated from a soybean CC embryo (26 days after flowering) cDNA library. The invention CC embryo (26 days after flowering) cDNA library. The invention CC encoding cyclin A, cyclin delta-1, cyclin delta-2 and cyclin delta-3 CC polypeptides (see AAV31889-902). It also relates to the construction CC of chimeric genes encoding all or a portion of a cyclin, in sense CC ensults in altered levels of the cyclin protein in a transformed CC ensults in altered levels of the cyclin protein in a transformed CC ell division in those cells. The nucleic acid fragments may be CC used to express cyclins in plant cells to enhance cell tissue CC culture growth. The availability of nucleic acid sequences encoding CC ellurare growth. The availability of nucleic acid sequences encoding CC culture, increase the efficiency of gene transfer and help provide more stable transformations. The proteins can be used as targets CC enzymes that may be useful as herbicides.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     seq_name: /SIDS2/gcgdata/geneseq/geneseqn/NA1999.DAT:AAZ19959
                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 7; Page 53-54; 68pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New isolated plant cyclin genes, used to develop products for use herbicides and for developing plant breeding programs - \,
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US-09-530-209A-2 x AAZ19959
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                                                                                                                                  ....LeuGlnLysGluArgValLysLysIleGlyGluMetIleGluSe
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seq_documentation_block:
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Quality:
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US-09-530-209A-2 x AAV33885
Align seg 1/1 to: AAV33885
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CDC; RD; retinoblastoma; germination; flowering; seed; fruit;
root development; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  N. tabacum CYCD3;1 gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         25-JAN-1999 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAV33885;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAV33885 standard; cDNA to mRNA; 1679 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   296 LysThrHisAspSerSerSerSerTyrThrHisLeuSer 308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            806 TGCGAGTGACAATATCTCGGCCCCATTATGAGGTCTAGTGTCTCATCCTTC 855
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          756 ACTTGTGATTGACAATAACCAGAGGAAACCCCCTAAGGTGTTACCACAGC 805
                                                                                                                                                                                                                                                                                This sequence represents the CYCD3;1 cDNA from Nicotiana tabacum which encodes a D-type cyclin. The sequence can be used to alter the growth characteristics or architecture of plants by altering the (functional) level in the plant cells of a cell-division controlling protein that can bind to, or phosphorylate, an Rb-like protein, such as a D-type cyclin. Modulation of the cyclin gene is used to increase or decrease the growth rate, provide faster germination, reduce time to flowering, increase the number of flowers, seeds or fruits per plant, increase root development, reduce height and to delay flowering in a range of plants, e.g. legumes, grasses, malze, oilseed rape, wheat, tomato, rice, barley, sunflower, carrattenom.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Regulating growth and structure of plants by modulating protein that controls cell division - specifically a D-type cyclin, and related chimeric genes and transformed cells and plants, used to alter growth rate, flowering, seed production etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-OCT-1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 1998-532012/45.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Murray JAH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           26-MAR-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  24-MAR-1998;
                                                                                                                                                                                                                            Sequence 1679 BP; 537 A; 281 C; 293 G; 568 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 14; p54; 75pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (UYCA-) UNIV CAMBRIDGE TECH SERVICES LTD.
                                                                                                                                                                                                                                                                   carnation, chrysanthemum,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TTAGCATCATCCTTCACCTTCATCATCCTCTTTGTCT 894
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .....valSerAlaCysCysPheSerPhe 295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           97EP-0302096
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                                                                                                         379.00
1.805
57.692
        from: 1
                                                                                                       Length:
Gaps:
Percent Identity:
                                                                                                                                                                                                                                                                          rose,
                                                                                                                                                                                                                                                                          tulip, etc.
        to: 1679
                                                                                                              364
17
31.044
                                                                                                                                                                                                                                     0 other;
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XXX DEXX

260	243 989	229 939	213 901	196 875	190 825	174 775	157 725	140 675	12 4 625	107 575	90 525	74 475	57 440	42 390	33 340	24 298	13 249	4 199
) LysGluArgValLysLysTleGlyGluMetTleGluSerAspGlySerAs 2	rgValHisPheAspAsnSerSerPheSerProLeuPheSerLeuLeuGln 2 :::::: ::: CTGTTGACTACCAAAATCAACTTCTTGGGGTTCTCAAAATTAAC	aAlaAlaAlaValAlaLeuSerValSerGlyGluLeuGlnA ::: :::	ThrLysGlyIleAspPheLeuGluPheArgProSerGluAl :::::::: AGATTCGTACGTTATATGCCGTCTGTATT	ysAspGlnGluProScrAsnThrLeuIleSerArgSerLeuGinValIle 2 :::	UATGLYSMetSerLysC 1 : :::::::: AAGGAGGCTTGGGCTAAGAAATAATATTCACTGGGAATTTCTTAGAAGAT	LysTrpArgLeuArgAlaIleThrProCysSerTyrIleArgTyrPheLe 1 ::::: ::::::::::::::::::::::	heGluAlaLysSerValGlnArgMetGluLeuLeuValLeuAsnLysLeu 1 ::::::	rGluValProMetLeuIleAspLeuGlnValGlyAspProGlnPheValP 1 ::: ::: :::	GlnLeuLeuAlaYalAlaCysLeuSerLeuAlaAlaLysIleGluGluTh 1	spargPheLeuSerValHisAspLeuProSerGlyLysGlyTrpIleLeu 1	UValHisGlnPheGlyProLeuCysPheCysLeuAlaMetAsnTyrLeuA 10 :::: ::: ::: TTATTATGGTTTCTCTGCTTTGACTGCCGTTTTAGCCATAAATTACTTTG 57	D.:	euArgSerGlyAspLeuAsp 7 ::: CAAGATGACTCTTTA 4	GluSerGluGluIleIleMetGluMetValGluLysGluLysGlnH 57 ::: ::::	IleproGlnMetGlyPheSerGlnSer 4 ::: :: :::! ::: TTCTTTATTACCTTTGCTTTGGTAACAAGATTTATT 3	GluThr ACA	ValAspAspGluGlyMetIleV 2	GluasnLeuGluLeuSerLeuLeuCysth 13 :::
76	59			12	96		73 74	57 24	40 74	23	4 7	4	42	9	9	9	7	8

us-09-530-209A-2 x AAV33886

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alignment_scores:
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ID AAV33886 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                seq_name: /SIDS2/gcgdata/geneseq/geneseqn/NA1998.DAT:AAV33886
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1033
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1121 ATAGCCCAAGTGGTGATTGATCCA.....ATTTACAGTTCAGAA 1161
                                                                                                                                                                                                                                    This sequence represents the CYCD3;2 cDNA from Nicotiana tabacum which encodes a D-type cyclin. The sequence can be used to alter the growth characteristics or architecture of plants by altering the (functional) level in the plant cells of a cell-division controlling protein that can bind to, or phosphorylate, an Rb-like protein, such as a D-type cyclin. Modulation of the cyclin gene is used to increase or decrease the growth rate, provide faster germination, reduce time to flowering, increase the number of flowers, seeds or fruits per plant, increase root development, reduce height and to delay flowering in a range of plants, e.g. legumes, grasses, maize, oilseed rape, wheat, tomato, rice, barley, sunflower,
                                                                                                                                                              Sequence 1431 BP;
                                                                                                                                                                                                                   carnation, chrysanthemum, rose,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 14; p55-56; 75pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             growth rate, flowering, seed production etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Regulating growth and structure of plants by modulating protein controls cell division - specifically a D-type cyclin, and relat chimeric genes and transformed cells and plants, used to alter
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           D-type cyclin; growth; plant; cell-division control; phosphorylation; CDC; Rb; retinoblastoma; germination; flowering; seed; fruit;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         N. tabacum CYCD3;2 gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 25-JAN-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAV33886 standard; cDNA to mRNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (UYCA-) UNIV CAMBRIDGE TECH SERVICES LTD
Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AGTTCAAATGATTCATGGGATTTGGAGTCAACATCTTCATAT 1203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ThrHis.....AspSerSerSerTyr 304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ...ThrProAsnGlyValLeuGluValSerAlaCysCysPheSerPheLys
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                                                       Quality:
                           Ratio:
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                           370.50
1.992
     62.000
                                                                                                                                                              387 A;
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                                                                                                                                                              267 C;
  Percent
                                                                                                                                                                                                                   tulip, etc.
                                                                                                                                                              299 G; 478
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Identity:
                           Length:
Gaps:
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300
10
32.333
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PIXX

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Align seg 1/1
1103 TCAATCTGTACCTGGCAGTCCAAGTGGAGTTATCGATGCATATTTTAGTT
                                                                                                                                                        1005 ... AAAGTCAAACAGGATAGTTTTGAAGAATGCCATGATCTTATTCTAGAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                  214 erThrThrLysGlyIleAspPheLeuGluPheArgProSerGluAlaAla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              92 HisGlnPheGlyProLeuCysPheCysLeuAlaMetAsnTyrLeuAspAr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      58 uProSerAspAspTyrIleLysArgLeuArgSerGlyAspLeuAspLeuA 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      42 GluSerGluGluIleIleMetGluMetValGluLysGluLysGlnHisLe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ValProMetLeuIleAspLeuGlnValGlyAspProGlnPheValPheGl 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CTAATGGGCACTTCTGGCTACAATATCTGCCAAAGCCTCAAGCGCAAACA 1102
                                                                                                               MetIleGluSerAspGlySerAspLeuCysSerGln......
                                                                                                                                                                                             luArgValLysLys.....IleGlyGlu
                                                                                                                                                                                                                           lHisPheAspAsnSerSerPheSerProLeuPheSerLeuLeuGlnLysG
                                                                                                                                                                                                                                                                                                                  ACTGCAGTAGTGTATTTCGTGATCAATGAGATTGAGCCTTGCAATGCAAT
                                                                                                                                                                                                                                                                                                                                         AlaAlaValAlaLeuSerValSerGlyGluLeuGln.....ArgVa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ACGC.....CTCATT.....CTTGGTATTATCACTG
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                                      .....ThrProAsnGlyValLeuGluValSerAlaCysC
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1.2e-12

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Query length: 308
Database: MSSuper Patents NA:
Database sequences: 351203
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                                                                                                                                                                                                                                                                                                                                                                      /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:PCT-US93-05000-1
/cgn2_6/ptodata/2/ina/6A_COMB.seq:US-08-895-707-5 +
/cgn2_6/ptodata/2/ina/6A_COMB.seq:US-08-895-707-8 +
/cgn2_6/ptodata/2/ina/5A_COMB.seq:US-08-706-539-3 +
/cgn2_6/ptodata/2/ina/5B_COMB.seq:US-09-027-007-3 +
/cgn2_6/ptodata/2/ina/6B_COMB.seq:US-09-027-007-3 +
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/cgn2_6/ptodata/2/ina/5B_COMB.seq:US-09-092-770-7
                                                                                                                                                  /cgn2_6/ptodata/2/ina/5B_COMB.seq:US-08-480-912-1
/cgn2_6/ptodata/2/ina/6B_COMB.seq:US-09-027-007-1
                                                                                                                                                                                             /cgn2_6/ptodata/2/ina/5A_COMB.seq
/cgn2_6/ptodata/2/ina/5A_COMB.seq
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/cgn2_6/ptodata/2/ina/6B_COMB.seq
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; LOCATION:
US-08-464-517-3
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                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE:
16 TTGGCCATGGAGCTGCTGTGCCACGAGGTGGACCCGGTCCGCAGGGCCGT
                                      6 LeuGluLeuSerLeuLeuCysThrGluSerAsn......va
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
APPLICANT: BEACH, David H.
                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US 07/
FILING DATE: 16-OCT-1992
APPLICATION NUMBER: US 07/
FILING DATE: 26-MAY-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/
                                                                                                             INFORMATION FOR SEQ ID NO: 3:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC COMPA
OPERATING SYSTEM: PC-DV
SOFTWARE: ASCII(text)
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES: 5
                                                                                             SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
                                                                                                                                                  TELECOMMUNICATION INFORMATION: TELEPHONE: (617) 227-7400
                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/08/464,517 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDIUM TYPE: Floppy disk
                                                                                                                                                                                          REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                          REGISTRATION NUMBER:
                                           nucleic acid
                                                                                                                                                                                                                          Matthew P. Vincent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       60 State Street
                                                                                                                                   (617) 227-5941
                   linear
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SYSTEM: PC-DOS/MS-DOS
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FILING DATE: 16-0CT-192
APPLICATION NUMBER: US 07/888,178
FILING DATE: 26-MAY-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/701,514
FILING DATE: 16-MAY-1991
ATTORNEY/AGENT INFORMATION:
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TELEFAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: 3:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII(text)
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: BEACH, David H.
TITLE OF INVENTION: D-TYPE CYCLIN AND USES RELATED THERETO
NUMBER OF SEQUENCES: 50
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
LENGTH: 1970 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEPHONE: (617) 227-7400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY:
ZIP: 021
                                                                113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STREET: 60 S
CITY: Boston
                                                                                                                                                                                                 16 TTGGCCATGGAGCTGCTGTGCCACGAGGTGGACCCGGTCCGCAGGGCCGT 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Matthew P. Vincent REGISTRATION NUMBER: 36, REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE:
                                                                                                 34
                                                                                                                                  66
                                                                                                                                                              17 lAspAspGluGlyMetIleValAspGluThrProIleGluIleSerIleP
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                                 48
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRANDEDNESS:
                                                                                                                                                                                                                                  9
roGlnMetGlyPheSerGlnSerGluSerGluGluIleIle.......47
                                                                                                                                GCGGGACCGCAACCTGCTCGGAGACGACCGCGTCCTGCAG...AACCTGC 112
                                                                                                                                                                                                                                LeuGluLeuSerLeuLeuCysThrGluSerAsn......va
                                                                TCACCATCGAATTCCCGCCGGGCTTGGCCATGGAGCTGCTGTGCCACGAG 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               02109
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62.752
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            212
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                                                                                                                                                                           sq_documentation_block:
Sequence 3, Application PC/TUS9305000
GENERAL INFORMATION:
APPLICANT: MITOTIX
TITLE OF INVENTION: D-Type Cyclin and
NUMBER OF SEQUENCES: 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  209
                                                                                                                                                     CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                    268 luMetIleGluSer.AspGlySerAspLeuCysSerGlnThr 281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         774
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         674 CACCGTCGATGATCGCAACTGGAAGTGTGGGAGCAGCCATCTGTGGGCTC 723
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  624 TCAGACCTTCATTGCTCTGTGTGCCACCGACTTTAAGTTTGCCATGTACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                580
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    193 MetSerLysCysAspGlnGluProSerAsnThrLeuIleSerArgSerLe 209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     176
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            351 GGTCCCGACTCCGAAGTCCCAT...CTGCAACTCCTGGGTGCTGTCTGCA 397
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         114 pLeuProSerGlyLysGlyTrpIleLeuGlnLeuAlaValAlaCysL 131 :::|||::: |||::: |||:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           307 GTCTTCCCTCTGGCCATGAATTACCTGGACCGTTTCTTGGCT.....GG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           257
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COMPUTER READABLE FORM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        148 LeuGlnValGlyAspProGlnPheValPheGluAlaLysSerValGlnAr 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       81
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                     COUNTRY: U
ZIP: 02173
                                                                      STATE:
                                                                                         CITY:
                                                                                                          STREET:
                                                                                                            ADDRESSEE: Hamilton, Brook, Smith & STREET: Two Militia Drive
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         uGlnVal...IleAlaSerThrThrLysGlyIleAspPheLeuGluPheA 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               rgLeuArgAlaIleThrProCysSerTyrIleArgTyrPheLeuArgLys 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TGTTCCTGGCCTCCAAACTCAAAGAGACCAGC...CCCCTG......435
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CysPheCysLeuAlaMetAsnTyrLeuAspArgPheLeuSerValHisAs 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TGGCCACCTGGATGCTGGAGGTCTGTGAGGAACAGAAGTGCGAAGAAGAG
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                                                                                                                                                                                                                                                                                                                                                                                          ACCAGATTGAGGCGGTGCTCCTCAATAGCCTGCAGCAGTACC 865
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GCTGGCTAAGATCACCAACACAGACGTGGATTGTCTCAAAGCTTGCCAGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CTGCCCCAG.....CAGCGGGAGAAGCTGTCTCTGATCCGCAAGCATGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ....ACCGCGGAGAAGCTGTGCATTTACACCGACAACTCCATCAAGCC 479
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  laLeuAsnTrpIleTrpLysAlaCysGluValHisGlnPheGlyProLeu 97
                                                              Lexington : Massachusetts
                                                                                                                                  Reynolds, P.C
                                                                                                                                                                                                     Uses Related Thereto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  673
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; STRANDEDNESS:
; TOPOLOGY: line
; MOLECULE TYPE: I
PCT-US93-05000-3
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US-09-530-209A-2 x PCT-US93-05000-3
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Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Align seg 1/1 to: PCT-US93-05000-3 from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ratio:
Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: 616-861-9540 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/05000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/888,178
FILING DATE: 26-MAY-1992
ATTORNEY/ACENT INFORMATION:
NAME: Granahan, Patricia
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              163
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                                                                                                                                                                                                                                                                             257
                                                                                                                                                                                                                                                                                                                                                                   213 CAAGTGCGTGCAGAAG...GACATCCAACCCTACATG...CGCAGAATGG 256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      113 TCACCATCGAATTCCCGCCGGGCTTGGCCATGGAGCTGCTGTGCCACGAG 162
                                                                                                                                                                                                                                                                                                                                                                                                            64 eLysArgLeuArgSerGlyAspLeuAspLeuAsnValGlyArgArgAspA 81
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Granahan, Patricia
REGISTRATION NUMBER: 32,227
REFERENCE/DOCKET NUMBER: CS
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CLASSIFICATION:
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                                                                                                                                                                           laLeuAsnTrpIleTrpLysAlaCysGluValHisGlnPheGlyProLeu 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TTGGCCATGGAGCTGCTGTGCCACGAGGTGGACCCGGTCCGCAGGGCCGT 65
                            euSerLeuAlaAlaLysIleGluGluThrGluValProMetLeuIleAsp 147
:: |||||:::||||:::||||||:::
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MetGluMetValGluLysGluLysGlnHisLeuProSerAspAspTyrIl 64
TGTTCCTGGCCTCCAAACTCAAAGAGACCAGC...CCCCTG.....
                                                                                     GGTCCCGACTCCGAAGTCCCAT...CTGCAACTCCTGGGTGCTGTCTGCA 397
                                                                                                                                pLeuProSerGlyLysGlyTrpIleLeuGlnLeuLeuAlaValAlaCysL 131
                                                                                                                                                                                                                                                                           TGGCCACCTGGATGCTGGAGGTCTGTGAGGAACAGAAGTGCGAAGAAGAG 306
                                                                                                                                                                                                                                                                                                                                                                                                                                                              GTGGACCCGGTCCGCAGGGAGGAGCGCTACCTTCCGCAGTGCTCCTACTT 212
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62.752
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seq_name: /cgn2_6/ptodata/2/ina/5A_COMB.seq:US-08-306-691B-51
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Calabretta
APPLICANT: Skorski, To
TITLE OF INVENTION: A
TITLE OF INVENTION: O
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              209
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  241 LeuGlnArgValHisPheAspAsnSerSerPheSerProLeuPheSerLe 257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              674 CACCGTCGATGATCGCAACTGGAAGTGTGGGAGCAGCCATCTGTGGGCTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     624 TCAGACCTTCATTGCTCTGTGTGCCACCGACTTTAAGTTTGCCATGTACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                193 MetSerLysCysAspGlnGluProSerAsnThrLeuIleSerArgSerLe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                176 rgLeuArgAlaIleThrProCysSerTyrIleArgTyrPheLeuArgLys 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                480 TCAGGAGCTGCTGGAGTGGGAACTGGTGCTGGGGGAAGTTGAAGTGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     164 gMetGluLeuLeu............ValLeuAsnLysLeuLysTrpA 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              148
NAME: MONACO, Daniel A.
REGISTRATION NUMBER: 30,480
REFERENCE/DOCKET NUMBER: 8321-8
TELECONMUNICATION INFORMATION:
TELEPHONE: (215) 568-8383
                                                                                                                                                                                                                                                                COMPUTER: IBM PS/2
OPERATING SYSTEM: MS-DOS
SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
                                                                                                                                                                           CLASSIFICATION: 514
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES: 5
                                                                                  ATTORNEY/AGENT INFORMATION:
NAME: Monaco, Daniel A.
                                                                                                                                                                                                    APPLICATION NUMBER: US/08/3
FILING DATE: September 15,
CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                STREET: Two Penn Center, Suite 1800
CITY: Philadelphia
STATE: non----
                                                                                                                                                                                                                                                                                                                                                                                                STATE: Pennsylvania COUNTRY: U.S.A. ZIP: 19102
                                                                                                                                    FILING DATE:
                                                                                                                                                         APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LeuGlnValGlyAspProGlnPheValPheGluAlaLysSerValGlnAr 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     rgProSerGlu...AlaAlaAlaAlaValAlaLeuSerValSerGlyGlu 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       uGlnVal...IleAlaSerThrThrLysGlyIleAspPheLeuGluPheA 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CTGCCCCAG.....CAGCGGGAGAAGCTGTCTCTGATCCGCAAGCATGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ACCTGGCAGCTGTCACTCCTCATGACTTCATTGAGCACATCTTGCGCAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ACCAGATTGAGGCGGTGCTCCTCAATAGCCTGCAGCAGTACC 865
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              uLeuGlnLys......GluArgValLysLysIleGlyG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ....ACCGCGGAGAAGCTGTGCATTTACACCGACAACTCCATCAAGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           luMetIleGluSer.AspGlySerAspLeuCysSerGlnThr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GCTGGCTAAGATCACCAACACAGACGTGGATTGTCTCAAAGCTTGCCAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Calabretta, Bruno
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ANTISENSE OLIGONUCLEOTIDES TARGETING COOPERATING
                                                                                                                                                                                                                                                US/08/306,691B
                                                                                                                                                                                                                           1994
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alignment_scores:
    Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-08-306-691B-51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      alignment_block:
US-09-530-209A-2 x US-08-306-691B-51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; TELEX: NO. 5734039e
INFORMATION FOR SEQ ID NO: 51:
SEQUENCE CHARACTERISTICS:
LENGTH: 1325 base Type:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Align seg 1/1 to: US-08-306-691B-51 from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   145 ATGGAACACCAGCTCCTGTGCTGCGAAGTG......
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    397
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         253 ACCTGCGCGCCCTCGGTGTCCTACTTCAAATGTGTGCAGAAGGAGGTCCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        175
                                                                                                                                                                                                                                                                                                                                                           139 luThrGluValProMetLeuIleAspLeuGlnValGlyAspProGlnPhe 155
                                                                                                                                                                                                                                                                                                                                                                                                                                      122 eLeuGlnLeuLeuAlaValAlaCysLeuSerLeuAlaAlaLysIleGluG 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        106
                                                                                                                                                               585 GCTCAAGTGGAACCTGGCCGCAATGACCCCGCACGATTTCATTGAACACT
                                                                                                                                                                                      172 SLeuLySTrpArgLeuArgAlaIleThrProCysSerTyrIleArgTyrP 189
                                                                                                                                                                                                                                          535 TCCATCCGGCCCGAGGAGCTGCTGCAAATGGAGCTGCTCCTGGTGAACAA 584
                                   206 SerArgSerLeuGlnVal...IleAlaSerThrThrLysGlyIleAspPh 221
                                                                                                                 189 heLeuArgLysMetSerLysCysAspGlnGluProSerAsnThrLeuIle 205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                39
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679 CGCAAACACGCGCAGACCTTCGTTGCCTCTTGTGCCACAGATGTGAAGTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        89
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6 LeuGluLeuSerLeuLeuCysThrGluSerAsnValAspAspGluGlyMe
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ysGluValHisGlnPheGlyProLeuCysPheCysLeuAlaMetAsnTyr 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               uAspLeuAsnValGlyArgArgAspAlaLeuAsnTrpIleTrpLysAlaC
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                                                                                                                                                                                                                                                                                                                          AGACC...ATCCCCCTGACGCCGAGAAGCTGTGCATCTACACCGACGGC 534
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CTGGACCGCTTCCTGTCGCTGGAGCCCGTGAAAAAAGAGCCGC.....
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GCCGTCCATG.....CGGAAGATCGTCGCCACCTGGATGCTGGAGGTCT
                                                                               TCCTCTCCAAAATGCCA.....GAGGCGGAGGAGAACAAACAGATCATC
                                                                                                                                                                                                                                                                                                                                                                                                   Ratio:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     to: 1325
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280	266 leGlyGluMetIleGluSerAspGlySerAspLeuCysSerGln ::::::: ::: ::: ::::::::::::::	
266 3003	249 rSerPheSerProLeuPheSerLeuLeuGlnLysGluArgValLysLysI	
249 2960	233 ValAlaLeuSerValSerGlyGluLeuGlnArgValHisPheAspAsnSe :::: ::: 2928 GTGGTGGCCGCAGTGCAAGGCCTGAACCTGAGG	
232 2927	217 ysGlyIleAspPheLeuGluPheArgProSerGluAlaAlaAlaAla :::	
217 2877	201 rAsnThrLeuIleSerArgSerLeuGlnValIleAlaSerThrThrL :::	
201 2827	185 TyrlleArgTyrPheLeuArgLysMetSerLysCysAspGlnGluProSe ::: ::::: 2784 TTCATTGAACACTTCCTCTCCAAAATGCCAGAGGCGGAGGAGAA	
184 2783	168 euValLeuAsnLysLeuLysTrpArgLeuArgAlaIleThrProCysSer ::::: :: ::	
168 2733	156 lPheGluAlaLysSerValGlnArgMetGluLeuL::::::::::::::::::::::::::::::::::	
156 2683	140 ThrGluValProMetLeuIleAspLeuGlnValGlyAspProGlnPheVa :: :: :::::::: 2652 ACCATCCCCCTGACGGCCGAGAAGCTGTGCAT	
139 2651	123 euGlnLeuLeuAlaValAlaCysLeuSerLeuAlaAlaLysIleGluGlu ::::::: ::::::: :::::	
123 2601	106 uAspArgPheLeuSerValHisAspLeuProSerGlyLysGlyTrpIleL 	
106 2560	90 GluValHisGlnPheGlyProLeuCysPheCysLeuAlaMetAsnTyrLe :::::: 	
89 2510	73 spieuAsnValGlyArgArgAspAlaLeuAsnTrpIleTrpLysAlaCys :::::: :::::: 2467 CGTCCATGCGGAAGATCGTCGCCACCTGGATGCTGGAGGTCTGC	
73 2466	56 nHisLeuProSerAspAspTyrIleLysArgLeuArgSerGlyAspLeuA	
56 2416	40 GlnSerGluSerGluGluIleIleMetGluMetValGluLysGluLysGluLysGluLysGluLysGluLysGluLysGluLysGluLysGluLysGluLysGluLysGluLysGluLysGluCysGluGluGluGluGluGluGluGluGluGluGluGluGluG	
39 2375	23 leValAspGluThrProIleGluIleSerIleProGlnMetGlyPheSer	
23	6 uGluLeuSerLeuLeuCysThrGluSerAsnValAspAspGluGlyMetI 	
6 2308	1 MetalaGluGluAsnLe	
	Align seg 1/1 to: US-08-770-761A-1 from: 1 to: 4621	

nd	Sequence 7, Application US/08472893A PATENT NO. 5677130 GENERAL INFORMATION: APPLICANT: Meeker, Timothy C. TITLE OF INVENTION: BC1-1 Locus Nucleic Acid TITLE OF INVENTION: Assay Methods NUMBER OF SEQUENCES: 10 CORDETENDENT ADDRESS:
7	_name: /cgn2_6/ptodata/2/ina/5A_COMB.seq:US-08-472-893A- documentation_block:
280 886	265 sIleGlyGluMetIleGluSerAspGlySerAspLeuCysSerG ::::::::::: ::: ::: 837 CCTCTCCAGAGTGATCAAGTGTGACCCGGACTGCCTCCGGGCCTGCCAGG
	249 SerSerPheSerProLeuPheSerLeuLeuGlnLySGluArgValLySLy
4 9	232 laValAlaLeuSerValSerGlyGluLeuGlnArgValHisPheAspAsn :: ::: ::: ::: 761 GCGTGGTGGCCGCAGTGCAAGGCCTGAACCTGAGG
. σ ω	euGluPheArgProSerGluAlaAlaAla :::::
1 1	201 SerAsnThrLeuIleSerArgSerLeuGlnValIleAlaSerThrTh :::::: ::: :::
60	184 erTyrIleArgTyrPheLeuArgLysMetSerLysCysAspGlnGluPro ::::: ::::: 617 aTTTCATTGAACACTTCCTCCAAAATGCCAGAGGCGGAGGAG
1 8	167 uLeuValLeuAsnLysLeuLysTrpArgLeuArgAlaIleThrProCysS
9 9	gMetGluL : AATGGAGC
	139 luThrGluValProMetLeuIleAspLeuGlnValGlyAspProGlnPhe :: ::
	122 eLeuGlnLeuLeuAlaValAlaCysLeuSerLeuAlaAlaLysTleGluG
ωΝ	
105 393	AsnTyr AACTAC
89 343	72 uAspLeuAsnValGlyArgArgAspAlaLeuAsnTrplleTrpLysAlaC (
72 299	56 GlnHisLeuProSerAspAspTyrIleLysArgLeuArgSerGlyAspLe 7 ::: :::::::::::::::::::::::
	209 TCAACGACCGGGTGCTGCGGGCCATGCTGAAGGCGGAGGAG 2

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alignment_scores:
Quality:
Ratio:
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US-09-530-209A-2 x US-08-472-893A-7
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                                                                                                                                                                                                                                                                                                                                                                                                          Align seg 1/1 to: US-08-472-893A-7 from: 1 to: 4221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STATE: CA
COUNTRY: USA
ZIP: 94105
ZIP: 94105
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA: US/08/472,893A
FILING DATE: U7-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/947,120
FILING DATE: 17-SEP-1992
ATTORNEY/AGENT INFORMATION:
NAME: Lauder, Leona L.
                                                               300 GCCGTCCATG.....CGGAAGATCGTCGCCACCTGGATGCTGGAGGTCT 343
                                                                                                                                                                                           209 TC.....AACGACCGGGTGCTGCGGGCCATGCTGAAGGCGGAGGAG 249
                                                                                                                                                                                                                                                                                                                                   250 ACCTGCGCGCCCTCGGTGTCCTACTTCAAATGTGTGCAGAAGGAGGTCCT 299
                                                                                                                                                                                                                                                                     172 .....GAAACC...ATCCGCCGCGCGTACCCCGATGCCAACCTCC 208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: CI
 344
               89 ysGluValHisGlnPheGlyProLeuCysPheCysLeuAlaMetAsnTyr 105
                                                                                               72 uAspLeuAsnValGlyArgArgAspAlaLeuAsnTrpIleTrpLysAlaC 89
                                                                                                                                                               56 GlnHisLeuProSerAspAspTyrIleLysArgLeuArgSerGlyAspLe 72
                                                                                                                                                                                                                         6 LeuGluLeuSerLeuLeuCysThrGluSerAsnValAspAspGluGlyMe 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: CDS
LOCATION: 142..1026
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: Leona L. Lauder
STREET: Steuart Street Tower, 18th Fl., One Market
STREET: Plaza
CITY: San Francisco
GCGAGGAACAGAAGTGCGAGGAGGAGGTCTTCCCGCTGGCCATGAACTAC 393
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            236.00
1.349
59.727
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length: 293
Gaps: 13
Percent Identity: 28.669
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		TGTCGCTGGAGGCCGTGAAAAGAGGCCGTGAAAAAGAGCCGTGAAAAAAGAGCCCGTGAAAAAAGAGCCCGTGAAAAAAAGAGCCGTGAAAAAAAA	euserValHisAspLeuProSerGlyLy	TGTCGCTGGAGCCCGTGAAAAAGAGCCCTGAAAAAAGAGCCACTTGCATGTCGTGGCCTGGAGCCTGCAGCCTTGCATGTCGTGCCTTGCATGTCTTCGTTCG	#	TGTCGCTGGAGCCCGTGAAAAAAAAAAAAAAAAAAAAAA	EUSETValHisAspLeuP ::::::::::::::::::::::::::	EUSETValHisAspLeuP ::::::::::::::::::::::::::	EUSETValHisAspLeuP ::::::::::::::::::::::::::	EUSETValHisAspLeuP ::::::::::::::::::::::::::	EUSETValHisAspLeuP ::::::::::::::::::::::::::	EUSETValHisAs :::::: :::::: : ::::::: : ::::::	RISERVALHI	RISERVALHI	RISERVALHI	BeuServalH ::: TGTCGCTGG AlaValAla GGGGCCACT GGGGCCACT CCTGCTGCT CCTGCTCACC CTTCCTCTCT CCTCCTCTCT CCTCCTCTCTCT	REUSERVA AlaValA ACCCCT CCTTCCTC TTCCATTT TTCCATTT TTCCATTT TTCCATTT TTCCATTT TTCCATCT TTCCATTT TTCCATCT TTCCATCT TTCCATTT TTCATTT TTCATT TTCATTT TTCATTT TTCATTT TTCATTT TTCATTT TTCATTT TTCA	PGTCGC RGGGGCC CCTG CCTG CCTGC	**************************************	Jedas	Jedas	Jeug.	Jeug.	Jeug.	106 LeuAs 1394 CTGGAV 112 eLeuG; 436 .CTGGAV 139 luThre 485 AGACC 156 VALPhe :::::: 517 ATCTAV 167 LLeuV 167 LLeuV 167 LLeuV 167 ACCAG 167 ATTTY 184 erTyr 184 erTyr 184 erTyr 187 ACCAG 201 SerAs 661 AACAA 216 rLysG 711 CACAG 216 rLysG 711 CACAG 216 rLysG 711 CACAG 218 SerSe 711 CACAG 232 LaVal 1761 GCGTG 249 SerSe 7761 GCGTG 249 SerSe 7761 GCGTG 771 CACAG 278 ACCAG 2796 280 InThr 1887 AGCAG 280 InThr 280 InThr 280 InThr 287 AGCAG 277 CTCTT 280 InThr 287 AGCAG 277 STREET: COMPUTER MEDIUM CO			
		TGTCGCTGGAGGCCGTGAAAAGAGGCCGTGAAAAAGAGCCGTGAAAAAAGAGCCCGTGAAAAAAGAGCCCGTGAAAAAAAGAGCCGTGAAAAAAAA	euserValHisAspLeuProSerGlyLy	TGTCGCTGGAGCCCGTGAAAAAGAGCCCTGAAAAAAGAGCCACTTGCATGTCGTGGCCTGGAGCCTGCAGCCTTGCATGTCGTGCCTTGCATGTCTTCGTTCG	#	TGTCGCTGGAGCCCGTGAAAAAAAAAAAAAAAAAAAAAA	EUSETValHisAspLeuP ::::::::::::::::::::::::::	EUSETValHisAspLeuP ::::::::::::::::::::::::::	EUSETValHisAspLeuP ::::::::::::::::::::::::::	EUSETValHisAspLeuP ::::::::::::::::::::::::::	EUSETValHisAspLeuP ::::::::::::::::::::::::::	EUSETValHisAs :::::: :::::: : ::::::: : ::::::	RISERVALHI	RISERVALHI	RISERVALHI	BeuServalH ::: TGTCGCTGG AlaValAla GGGGCCACT GGGGCCACT CCTGCTGCT CCTGCTCACC CTTCCTCTCT CCTCCTCTCT CCTCCTCTCTCT	REUSERVA AlaValA ACCCCT CCTTCCTC TTCCATTT TTCCATTT TTCCATTT TTCCATTT TTCCATTT TTCCATCT TTCCATTT TTCCATCT TTCCATCT TTCCATTT TTCATTT TTCATT TTCATTT TTCATTT TTCATTT TTCATTT TTCATTT TTCATTT TTCA	PGTCGC RGGGGCC CCTG CCTG CCTGC	**************************************	Jedas	Jedas	Jeug.	Jeug.	Jeug.	106 LeuAs 1394 CTGGAV 112 eLeuG; 436 .CTGGAV 139 luThre 485 AGACC 156 VALPhe :::::: 517 ATCTAV 167 LLeuV 167 LLeuV 167 LLeuV 167 ACCAG 167 ATTTY 184 erTyr 184 erTyr 184 erTyr 187 ACCAG 201 SerAs 661 AACAA 216 rLysG 711 CACAG 216 rLysG 711 CACAG 216 rLysG 711 CACAG 218 SerSe 711 CACAG 232 LaVal 1761 GCGTG 249 SerSe 7761 GCGTG 249 SerSe 7761 GCGTG 771 CACAG 278 ACCAG 2796 280 InThr 1887 AGCAG 280 InThr 280 InThr 280 InThr 287 AGCAG 277 CTCTT 280 InThr 287 AGCAG 277 STREET: COMPUTER MEDIUM CO			
Itell	Itell			ILEULEUALAVALHISASPLEUPROSERGIYI		TICCTTCCTGTCGCTGGAGCCCGTGAAAAAAAAAAAAAAA	ILEULEUAL AVAILACYSLEUSER ILEULEUAL AVAILACYSLEUSER ILEULEUAL AVAILACYSLEUSER ILEULEUAL AVAILACYSLEUSER ILEULEUAL AVAILACYSLEUSER ILEULEUAS ILEULEUA ILEAS PLEUGI ::: :::: :::: CCGACCACTTCCATTCCATTCCATGTTC ILEULEUAS ILYS ERVAGGCCCAAGGCCCCAAGGCCCCAAGGCTCAAGTGGAACCCTG GAGACAACTTCCTCCTCCAAGTGGAACCCTG ILEULIESER ILIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	ILEULEUAL AVAILACYSLEUSER ILEULEUAL AVAILACYSLEUSER ILEULEUAL AVAILACYSLEUSER ILEULEUAL AVAILACYSLEUSER ILEULEUAL AVAILACYSLEUSER ILEULEUAS ILEULEUA ILEAS PLEUGI ::: :::: :::: CCGACCACTTCCATTCCATTCCATGTTC ILEULEUAS ILYS ERVAGGCCCAAGGCCCCAAGGCCCCAAGGCTCAAGTGGAACCCTG GAGACAACTTCCTCCTCCAAGTGGAACCCTG ILEULIESER ILIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	ILEULEUAL AVAILACYSLEUSER ILEULEUAL AVAILACYSLEUSER ILEULEUAL AVAILACYSLEUSER ILEULEUAL AVAILACYSLEUSER ILEULEUAL AVAILACYSLEUSER ILEULEUAS ILEULEUA ILEAS PLEUGI ::: :::: :::: CCGACCACTTCCATTCCATTCCATGTTC ILEULEUAS ILYS ERVAGGCCCAAGGCCCCAAGGCCCCAAGGCTCAAGTGGAACCCTG GAGACAACTTCCTCCTCCAAGTGGAACCCTG ILEULIESER ILIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	ILEULEUAL AVAILACYSLEUSER ILEULEUAL AVAILACYSLEUSER ILEULEUAL AVAILACYSLEUSER ILEULEUAL AVAILACYSLEUSER ILEULEUAL AVAILACYSLEUSER ILEULEUAS ILEULEUA ILEAS PLEUGI ::: :::: :::: CCGACCACTTCCATTCCATTCCATGTTC ILEULEUAS ILYS ERVAGGCCCAAGGCCCCAAGGCCCCAAGGCTCAAGTGGAACCCTG GAGACAACTTCCTCCTCCAAGTGGAACCCTG ILEULIESER ILIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	ILEULEUAL AVAILACYSLEUSER ILEULEUAL AVAILACYSLEUSER ILEULEUAL AVAILACYSLEUSER ILEULEUAL AVAILACYSLEUSER ILEULEUAL AVAILACYSLEUSER ILEULEUAS ILEULEUA ILEAS PLEUGI ::: :::: :::: CCGACCACTTCCATTCCATTCCATGTTC ILEULEUAS ILYS ERVAGGCCCAAGGCCCCAAGGCCCCAAGGCTCAAGTGGAACCCTG GAGACAACTTCCTCCTCCAAGTGGAACCCTG ILEULIESER ILIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	ILEULEUAL AVALABLES EVALHISAS	ILEULEUAL AVALABLES EVALUATED HISAS	ILEULEUAL AVALABLES EVALUATED HISAS	ILEULEUAL AVALABLES EVALUATED HISAS	ILEULEUALEVALHI	ILEULEUALEVALHI	ILEULEUALEVALHI		rgpheLeuServa	regPheLeuServ	BATTER FREE TREE COOKERN TO GET A COURT OF THE COURT OF T	ZHXVHH.ZHKDDXXX	ZHXVHH.ZHKDDXXX	18000000 2000000 0 0 0 0 0 0 0 0 0 0 0 0	ZHXDHH.ZHKBBXXX	1 H D D H H - 2 H K D B D O D D O D D O D O D D D D D D D D	106 Lei 194 CT 112 eLi 1436 . C 1436 . C 1436 . C 1436 . C 156 Va 15
pArgPheLeuSerValHisAspLeuProSerGlyLysG	pArgPheLeuSerValHisAspLeuProSerGlyLysG				pargpheLeuSerValHisAspLeuProSerGI	pargpheLeuSerValHisAspLeuProSerG(pArgPheLeuSerValHisAs	pArgPheLeuSerValHisAs	pArgPheLeuSerValHisAs	pArgPheLeuSerValHisAs	ppArgPheLeuSerValHi 	ppArgPheLeuSerValHi 	ppArgPheLeuSerValHi 	ppArgPheLeuSerValH	pArgPheLeuSerVa	ppArgPheLeuSerV		ZHXVHH.ZHKDDXXX	ZHXVHH.ZHKDDXXX	18000000 2000000 0 0 0 0 0 0 0 0 0 0 0 0	ZHXDHH.ZHKBBXXX	1 H D D H H - 2 H K D B D O D D O D D O D O D D D D D D D D	106 Lei 194 CT 122 eLi 1436 . C 1436 . C 1436 . C 1436 . C 156 Va 15

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; NAME/KEY: CDS
; LOCATION: 142..1026
US-08-947-492-7
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REGISTRATION NUMBER: 30,863
REFERENCE/DOCKET NUMBER: 91-210-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-777-9257
TELEPAX: 415-543-4219
INFORMATION FOR SEQ ID NO: 7:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08
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MOLECULE TYPE: cDI
HYPOTHETICAL: NO
FEATURE:
                                                                                                                                                                         394
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LENGTH: 4221 base pairs
TYPE: nucleic acid
485
                                                                                  106 LeuAspArgPheLeuSerValHisAspLeuProSerGlyLysGlyTrpI1 122
                                                                                                                                                                                                                                                                                                                                                 300 GCCGTCCATG......CGGAAGATCGTCGCCACCTGGATGCTGGAGGTCT 343
                                                                                                                                                                                                                                                                                                                                                                                                                                        250 ACCTGCGCGCCCTCGGTGTCCTACTTCAAATGTGTGCAGAAGGAGGTCCT 299
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ATTORNEY/AGENT INFORMATION:
                                       139 luThrGluValProMetLeuIleAspLeuGlnValGlyAspProGlnPhe 155
                                                                                                                                                                                                                                                              344 GCGAGGAACAGAAGTGCGAGGAGGAGGTCTTCCCGCTGGCCATGAACTAC 393
                                                                                                                                                                                                                                                                                       89 ysGluValHisGlnPheGlyProLeuCysPheCysLeuAlaMetAsnTyr 105
                                                                                                                                                                                                                                                                                                                                                                            72 uAspLeuAsnValGlyArgArgAspAlaLeuAsnTrpIleTrpLysAlaC 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             56 GlnHisLeuProSerAspAspTyrIleLysArgLeuArgSerGlyAspLe 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         39 erGlnSerGluSerGluGluIleIleMetGluMetValGluLysGluLys 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       22 tileValAspGluThrProileGluIleSerIleProGlnMetGlyPheS 39
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                                                                                                                                                                     CTGGACCGCTTCCTGTCGCTGGAGCCCGTGAAAAAGAGCCGC..... 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Quality:
Ratio:
.ATCCCCCTG...
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59.727
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Gaps: 13
Percent Identity: 28.669
  .ACGGCCGAGAAGCTGTGC 516
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	QUENCE CHARACTERISTICS: LENGTH: 4244 base pairs TYPE: nucleic acid STRANDEDNESS: single	· · · · · · · · · · · · · · · · · · ·	
	TELEPHONE: 202-371-2600 TELEFAX: 202-371-2540 RMATION FOR SEO ID NO: 1:	INF	
	STRATION NUMBER: 35, RENCE/DOCKET NUMBER:		
	FICATION: 435 /AGENT INFORMATIO	 A	
	APPLICATION NUMBER FILING DATE: 02-J		
	SOFTWARE: PatentIn Re	 G	
	MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible		
	COUNTRY: USA ZIP: 20005 COMPUTER READABLE FORM:	0	
	Washington DC	·. ·. ·.	
•	ESPONDENCE ADDRESS: DRESSEE: STERNE, KESSLER, GOLDSTEIN	Q:	
	PLIC TLE		
	entation_bio e 1, Applica No. 5858655 I INFORMATIO	Sequ Sequ Pate	
	: /cgn2_6/ptoda	eq_na	
	80 lnThrProAsnGlyValLeuGluValSer 289 :: ::::::::: 87 AGCAGATCGAAGCCCTGCTGCAGTCAAGC 915	28 88	
280 886	65 sileGlyGluMetIleGluSerAspGlySerAspLeuCysSerG ::::::::::: ::: :::	26 83	
836			
265	9 SerSerPheSerProLeuPheSerL	24	
248 795	2 laValAlaLeuSerValSerGlyGluLeuGlnArgValHisPheAspAsn :: ::: :: :::	23 76	
232 760	116 rLysGlyIleAspPheLeuGluPheArgProSerGluAlaAlaAlaA 	7:	
216 710	01 SerAsnThrLeuIleSerArgSerLeuGlnValIleAlaSerThrTh :::::::::::::::::::::::::::::::::	20 66	
200 660	84 erTyrlleArgTyrPheLeuArgLysMetSerLysCysAspClnGluPro ::::: ::::	18	
184 616	67 uLeuValLeuAsnLysLeuLysTrpArgLeuArgAlaIleThrProCysS	1¢ 5¢	
167 566	6 ValPheGluAlaLysSerValGlnArgMetGluLe ::::::::::::::::::::::::::::::::::::	156 517	

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alignment_block:
US-09-530-209A-2 x US-08-460-694-1
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; LOCATION:
US-08-460-694-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ratio:
Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Align seg 1/1 to: US-08-460-694-1 from: 1 to: 4244
                                                                                                                                                                                              623 ATTTCATTGAACACTTCCTCCCAAAATGCCA.....GAGGCGGAGGAG 666
                                                                                                                                                                                                                          523 ATCTACACCGACAACTCCATCCGGCCCGAGGAGCTGCTGCAAATGGAGCT 572
                                                                                                                                                                                                                                                                                                                                                                                                                           156 ValPheGluAlaLysSerValGln......ArgMetGluLe 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    491 AGACC...ATCCCCCTG......ACGGCCGAGAAGCTGTGC 522
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             122 eLeuGlnLeuLeuAlaValAlaCysLeuSerLeuAlaAlaLysIleGluG 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          400 CTGGACCGCTTCCTGTCGCTGGAGCCCGTGAAAAAGAGCCGC..... 441
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    215 TC.....AACGACCGGGTGCTGCGGGCCATGCTGAAGGCGGAGGAG 255
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                            216 rLysGlyIleAspPheLeuGluPheArgProSer...GluAlaAlaAlaA 232
                                                                                               667 AACAAACAGATCATCCGCAAACACGCGCAGACCTTCGTTGCCCTCTGTGC 716
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               139 luThrGluValProMetLeuIleAspLeuGlnValGlyAspProGlnPhe 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   306 GCCGTCCATG.....CGGAAGATCGTCGCCACCTGGATGCTGGAGGTCT 349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    256 ACCTGCGCGCCCTCGGTGTCCTACTTCAAATGTGTGCAGAAGGAGGTCCT 305
                                                                                                                                             201 SerAsnThrLeuIleSerArgSerLeuGlnVal...IleAlaSerThrTh 216
717 CACAGATGTGAAGTTCATTTCCAATCCGCCCTCCATGGTGGCAGCGGGGA 766
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        89 ysGluValHisGlnPheGlyProLeuCysPheCysLeuAlaMetAsnTyr 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              56 GlnHisLeuProSerAspAspTyrIleLysArgLeuArgSerGlyAspLe 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            72 uAspLeuAsnValGlyArgArgAspAlaLeuAsnTrpIleTrpLysAlaC 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  39 erGlnSerGluSerGluGluIleIleMetGluMetValGluLysGluLys 55
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148..1035
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Gaps: 13
Percent Identity: 28.669
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alignment_block: US-09-530-209A-2 x US-08-460-744-1 Align seg 1/1 to: US-08-460-744-1 from: 1 to: 4244	alignment_scores: Quality: 236.00 Length: 293 Ratio: 1.349 Gaps: 13 Percent Similarity: 59.727 Percent Identity: 28.669	INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS: LENGTH: 4244 base pairs TYPE: nucleic acid STRANDEDNESS: single TOPOLOGY: linear MOLECULE TYPE: CDNA FEATURE: NAME/KEY: CDS LOCATION: 1481035 US-08-460-744-1	ATION NUMBER O2-37 FICATION: 4 FICATION: 4 FICATION: 4 FICATION: 4 FICATION INFORMATION NUMBER ONCE/DOCKET NUMICATION IN 10 NO.E: 202-37	COUNTRY: USA ZIP: 20005 ; COMPUTER READABLE FORM: ; COMPUTER: Floppy disk ; COMPUTER: IBM PC compatible ; COMPUTER: IBM PC compatible ; OPERAPTING SYSTEM: PC-DOS/MS-DOS ; SOFTWARE: Patentin Release #1.0, Version #1.30 ; CURRENT APPLICATION DATA:	eq_documentati Sequence 1, A Patent NO. 61 GENERAL INFO APPLICANT: TITLE OF 1 NUMBER OF CORRESPONI ADDRESSE STREET: CITY: W STATE.	280 InThrProAsnGlyValLeuGluValSer 289 ::::::::: 893 AGCAGATCGAAGCCCTGCTGGAGTCAAGC 921 seq_name: /cgn2_6/ptodata/2/ina/6A_COMB.seq:US-08-460-744-1	9 SerSerPheSerProLeuPheSerLeuLeuGlnLysGluArgValLysLy	:: :::	232 tavatataLeuservatserGtyGtuLeuGtnArgvatHtsPneAspAsn 248
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6 LeuGluLeuSerLeuLeuCysThrGluSerAsnValAspAspGluGlyMe 22

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seq_documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                              seq_name: /cgn2_6/ptodata/2/ina/5A_COMB.seq:US-08-770-761A-4
                                                                                                                                                                                                                                                                                                                        Patent No. 5814503
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                              Sequence 4,
                                                                                                                                                           APPLICANT: Otto, Keith A.
APPLICANT: Rao, Ramachandra N.
TITLE OF INVENTION: FUSION PROTEINS COMPRISING CELL CYCLE
TITLE OF INVENTION: REGULATORY PROTEINS
UNMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 802
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    122
                                                                                                                                                                                                                                                                                                  APPLICANT:
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          89
                                                                                                     STREET: Lilly Corporate CITY: Indianapolis
                                              COUNTRY: UZIP: 46285
                                                                                                                                                  ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTTCATTGAACACTTCCTCCAAAATGCCA.....GAGGCGGAGGAG 666
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SerAsnThrLeuIleSerArgSerLeuGlnVal...IleAlaSerThrTh 216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   erTyrIleArgTyrPheLeuArgLysMetSerLysCysAspGlnGluPro 200
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               eLeuGlnLeuLeuAlaValAlaCysLeuSerLeuAlaAlaLysIleGluG 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CTGGACCGCTTCCTGTCGCTGGAGCCCGTGAAAAAGAGCCGC.....
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CCTCTCCAGAGTGATCAAGTGTGACCCAGACTGCCTCCGGGCCTGCCAGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AACAAACAGATCATCCGCAAACACGCGCAGACCTTCGTTGCCCTCTGTGC 716
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .CTGCAGCTGCTGGGGGCCACTTGCATGTTCGTGGCCTCTAAGATGAAGG
                                                                                                                                                                                                                                                                                                                                                                Application US/08770761A
                                                                                    IN
                                                                                                                              E: Eli Lilly and Company
Lilly Corporate Center/Patent Division
                                                                  USA
                                                                                                                                                                                                                                                                                                  Kovacevic, Steven
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alignment_scores:
Quality:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-530-209A-2 x US-08-770-761A-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: 317-277-1917 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2464 ACCTGCGCGCCCTCGGTGTCCTACTTCAAATGTGTGCAAAAGGAGGTCCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2423 TC.....AACGACCGGGTGCTGCGGGCCATGCTAAAGGCGGAGGAG
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2731 ATCTACACCGACAACTCCATCCGGCCCGAGGAGCTGCTGCAAATGGAGCT 2780
                                                                                      2699 AGACC...ATCCCCCTG.....
                                                                                                                                                                                                                                                                                                                                                                  2558 GCGAGGAACAGAAGTGCGAGGAGGAGGTCTTCCCGCTGGCCATGAACTAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                          2514 GCCGTCCATG.....CGGAAGATCGTCGCCACCTGGATGCTGGAGGTCT 2557
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CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                            TOPOLOGY: 11
MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
LENGTH: 4453 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELECOMMUNICATION INFORMATION: TELEPHONE: 317-376-0756
                                        156 ValPheGluAlaLysSerValGln.....ArgMetGluLe 167
                                                                                                                                 139 luThrGluValProMetLeuIleAspLeuGlnValGlyAspProGlnPhe
                                                                                                                                                                                                                     122 eLeuGlnLeuLeuAlaValAlaCysLeuSerLeuAlaAlaLysIleGluG 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   72 uAspLeuAsnValGlyArgArgAspAlaLeuAsnTrpIleTrpLysAlaC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    39 erGlnSerGluSerGluGluIleIleMetGluMetValGluLysGluLys 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 22 tileValAspGluThrProIleGluIleSerIleProGlnMetGlyPheS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6 LeuGluLeuSerLeuLeuCysThrGluSerAsnValAspAspGluGlyMe 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Gaylo, Paul J.
REGISTRATION NUMBER: 36
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: FILING DATE: 19-DE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: nucleic acid
STRANDEDNESS: sing
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                                                                                                                                                                                 .CTGCAGCTGCTGGGGGCCACTTGCATGTTCGTGGCCTCTAAGATGAAGG
                                                                                                                                                                                                                                                                       CTGGACCGCTTCCTGTCGCTGGAGCCCGTGAAAAAGAGCCGC.....
                                                                                                                                                                                                                                                                                                                                                                                                        ysGluValHisGlnPheGlyProLeuCysPheCysLeuAlaMetAsnTyr 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GlnHisLeuProSerAspAspTyrTleLysArgLeuArgSerGlyAspLe 72
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                                                                                      ACGGCCGAGAAGCTGTGC
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seq_name: /cgn2_6/ptodata/2/ina/5A_COMB.seq:US-08-770-761A-6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence b,
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                                                                           TELEFAX: 317-277-1917
INFORMATION FOR SEQ ID NO:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Otto, Keith A.
APPLICANT: Rao, Ramachandra N.
TITLE OF INVENTION: FUSION PRO
TITLE OF INVENTION: REGULATORY
NUMBER OF SEQUENCES: 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    265 sileGlyGluMetileGluSerAspGlySerAspLeu.....CysSerG 280
                                                                                                                                                                                                                                                                                      MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                            TELECOMMUNICATION INFORMATION:
                SEQUENCE CHARACTERISTICS:
LENGTH: 4540 base pairs
TYPE: nucleic acid
                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
NAME: Gaylo, Paul J.
REGISTRATION NUMBER: 36,808
REFERENCE/DOCKET NUMBER: X-
                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT:
                                                                                                                                                                                                                               APPLICATION NUMBER: US/08/770,761A FILING DATE: 19-DEC-1996 CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                                                                                                               STREET: Lilly Corporate: Indianapolis
STATE: IN
                                                                                                                                                                                                                                                                                                                                                                                                             ZIP: 46285
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                                                                                                                  TELEPHONE:
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Lilly Corporate Center/Patent Division
                                                                                              : 317-376-0756
317-277-1917
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                                                                             6:
                                                                                                                                                           x-10136
                                                                                                                                                                                                                                                                                                                   Version
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; TOPOLOGY: 1i
; MOLECULE TYPE:
US-08-770-761A-6
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                                                                                                                                                                                                                                                                                                                                                                                         156 ValPheGluAlaLysSerValGln.....ArgMetGluLe 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       139 luThrGluValProMetLeuIleAspLeuGlnValGlyAspProGlnPhe 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      22 tIleValAspGluThrProIleGluIleSerIleProGlnMetGlyPheS
                                                                                                                                                                                                                         167 uLeuValLeuAsnLysLeuLysTrpArgLeuArgAlaIleThrProCysS 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                39
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GCGAGGAACAGAAGTGCGAGGAGGAGGTCTTCCCGGCTGGCCATGAACTAC
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laValAlaLeuSerValSerGlyGluLeuGlnArgValHisPheAspAsn 248
                                                                                                                    AACAAACAGATCATCCGCAAACACGCGCAGACCTTCGTTGCCCCTCTGTGC
                                                                                                                                                                                                ATTTCATTGAACACTTCCTCCCAAAATGCCA.....GAGGCGGAGGAG
                                         CACAGATGTGAAGTTCATTTCCAATCCGCCCTCCATGGTGGCAGCGGGGA 2974
                                                                           rLysGlyIleAspPheLeuGluPheArgProSer...GluAlaAlaAlaA
                                                                                                                                                       SerAsnThrLeuIleSerArgSerLeuGlnVal...IleAlaSerThrTh 216
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Gaps:
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alignment_scores:
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                                                                                                                                                                                                                                                        US-08-246-361A-3
    Percent Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/963,308
FILING DATE: 16-0CT-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/888,178
FILING DATE: 26-MAY-1992
PRIOR APPLICATION DATA:
APPLICATION UMBER: US 07/701,514
FILING DATE: 16-MAY-1991
ATTORNEY/AGENT INFORMATION:
APPLICATION: NAME: NAME:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: (617) 227-59 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3101
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NUMBER OF SEQUENCES: 50
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 State Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION DATA:
APPLICATION NUMBER: US,
FILING DATE: 19-MAY-199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              265 sIleGlyGluMetIleGluSerAspGlySerAspLeu.....CysSerG 280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: BEACH, David H.
TITLE OF INVENTION: D-TYPE CYCLIN AND USES RELATED THERETO
                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STREET: 60 St
CITY: Boston
STATE: MA
                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: ... STRANDEDNESS: bui
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: ASCII(text)
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ZIP: 02109
                                                                                                                                                                                                                                                                                               NAME/KEY:
LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Matthew P. Vincent REGISTRATION NUMBER: 36,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: nucleic acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER: MII-004C
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Ratio:
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235.50
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    Percent Identity:
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29.153
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alignment_block:
US-09-530-209A-2 x US-08-246-361A-3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     573 CATTGCTCTGTGTGCCACCGACTTTAAGTTTGCCATGTACCCACCGTCGA 622
                                                                                                                                                                                                                                                                                                                                                                      212 .IleAlaSerThrThrLysGlyIleAspPheLeuGluPheArgProSerG
                                                                                                                                                                                                                                                                                                                                                                                                                                                        529
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        134 laAlaLysIleGluGluThrGluValProMetLeuIleAspLeuGlnVal 150
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723 GATCACCAACACAGACGTGGATTGTCTCAAAGCTTGCCAGGAGCAGATTG
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                                              .......GluArgValLysLysIleGlyGluMetIleG 271
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seq_name: /cgn2_6/ptodata/2/ina/5B_COMB.seq:US-08-464-517-1
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US-09-530-209A-2 x US-08-464-517-1
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;
;
LOCATION:
US-08-464-517-1
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APPLICATION NUMBER: US 07/963,308

APPLICATION NUMBER: US 07/963,308

APPLICATION NUMBER: US 07/888,178

APPLICATION NUMBER: US 07/888,178

PILING DATE: 26-MAY-1992

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/701,514

FILING DATE: 16-MAY-1991

ATTORNEY/AGENT INFORMATION:

NAME: Matthew P. Vincent

REGISTRATION NUMBER: 36,709

REFERENCE/DOCKET NUMBER: MII-004C

TELEPHONE: (617) 227-7400

TELEPHONE: (617) 227-740

TELEPAX: (617) 227-5941

INFORMATION FOR SEO ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 1325 base pairs

TYPE: nucleic acid

STPANTENNESS: double
                                                                                                                                                                                                                                                                                         alignment_scores:
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Sequence 1, Application US/08464517
Patent No. 5869640
GENERAL INFORMATION:
                                                                                                                                                                                                                               Quality:
Ratio:
Percent Similarity:
                                                                                                                                Align seg 1/1 to: US-08-464-517-1 from: 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: BEACH, David H.
TITLE OF INVENTION: D-TYPE CYCLIN AND USES RELATED THERETO NUMBER OF SEQUENCES: 50
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 State Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII(text)
CURRENT APPLICATION DATA:
                                                     FEATURE:
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ZIP: 02109
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CITY: Boston
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CLASSIFICATION: 435
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Gaps:
Percent Identity:
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10
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22	213	198	181	164	148	131	114	98	83	72	56	39	175
75	705	655	611	561	511	464	423	373	323	295	253	212	
9 laAlaAlaAlaValAlaLeuSerValSerGly 239	3 aSerThrThrLysGlyIleAspPheLeuGluPheArgProSerGluA 229	GINGluProSerAsnThrLeuIleSerArgSerLeuGlnValIleAl 213 Ill	hrproCysSerTyrIleArgTyrPheLeuArgLysMetSerLysCysAsp 197 ::::: :::: :::: ccccGcACGATTTCATTGAACACTTCCTCTCCAAAATGACAGAG 654		LeuGlnValGlyAspProGlnPheValPheGluAlaLysSerValGlnAr 164 ::::::::::::::::::::::::::::::::::::	euSerLeuAlaAlaLysIleGluGluThrGluValProMetLeuIleAsp 147 :: ::: ::: :::: ::: ::: TGTTCGTGGCCTCTAAGATGAAGGAGACCATCCCCCTGACGGCCGAG 510	pLeuProSerGlyLysGlyTrpIleLeuGlnLeuAlaValAlaCysL 131 ::: :::::::::::::::::::::::::::::::	CysPheCysLeuAlaMetAsnTyrLeuAspArgPheLeuSerValHisAs 114	AsnTrpIleTrpLysAlaCysGluValHisGlnPheGlyProLeu 97 :::: ::: ::::::: TCGCCACCTGGATGCTGGAGGTCTGCGAGGAACAGAAGTGCGAGGAGGAG 372	uAspLeuAsnValGlyArgArgAspAlaLeu82 :: GACGTCCTCCGTCCATGCCGAAGATCG 322	GlnHisLeuProSerAspAspTyrIleLysArgLeuArgSerGlyAspLe 72	erGlnSerGluSerGluGluIleIleMetGluMetValGluLysGluLys 55	

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9b_est2:BI140861

9b_est2:BG128122

9b_gss:CNS00U5S

9b_est2:BI203937

9b_est2:BI206090

9b_est2:BI206688

9b_est2:BI206688

9b_est2:BF096480

9b_est2:BF096480

9b_est2:BI204344
                                                                                                                                                                                                                                                                                                                   gb_est2:BG886881
gb_est1:A1812774
gb_est1:A036252
gb_est1:BE499582
gb_est2:B1270081
gb_est2:B6643290
gb_est2:B127073876
gb_est2:B1210187
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gb_est2:BG585934
gb_est1:BE642779
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gb_est1:AI728767
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gb_est2:BG125807
gb_est1:AV527915
gb_est2:BG128733
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Database ESTRS
Database Sequences: 11351937
Database length: 1077921985
Search time (sec): 1157.450000
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gb_est1:AI728683
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -WODEL-frame+_p2n.model -DEV=xlh
-Q-/cgn2_1/USPTO_spool/US09530209/runat_19012002_145800_20190/app_query.fasta_1.371
-Q-/cgn2_1/USPTO_spool/US09530209/runat_19012002_145800_20190/app_query.fasta_1.371
-DB=EST -QFMT=fastap -SUFFIX=rst -GAPOP=12.000 -GAPEXT=4.000
-MINMATCH=0.100 -LOOPCL=0.000 -LOOPEXT=0.000 -PGAPOP=4.500
-QGAPEXT=0.050 -XGAPOP=10.000 -XGAPEXT=0.500 -PGAPOP=6.000
-FGAPEXT=7.000 -YGAPOP=10.000 -YGAPEXT=0.500 -DELOP=6.000
-DELEXT=7.000 -START=1 -MATRIX=DLOSMIN62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0
-ALIGN=15 -MODE=LOCAL -OUTEMT=pfs -NORM=ext -HEAPSIZE=500
-MINLEN=0 -MAXLEN=200000000 -USER-US09530209_dCGN1 1_3954
-NCPU=6 -ICPU=3 -LONGLOG -DEV_TIMEOUT=120 -WARN_TIMEOUT=30
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1.2e-19
1.3e-19
3.4e-19
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. 8e-37
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                  AW623899
BI204344
                  EST321844
EST522384
                  tomato
                                   tomato nutri
                  Lycope
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gb_est1:AW704937
gb_est1:BE611087
gb_est1:AW671293
gb_est2:BG595229
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AUTHORS
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SOURCE
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JOURNAL
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seq_documentation_block:
LOCUS BG129531
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                                                                                                                                                                                                                                                                      Align seg 1/1 to: BG129531
                                                                                                                                                                                                                                                                                                          US-09-530-209A-2 x BG129531
                                                                                                                                                                                                                                                                                                                                                            Percent Similarity:
                                                                                                                                                                                               30 AGTGAAGAAAGCTTTTCTGTTATGTTGGAAAAGGAAAAAGTATTTTTACC
GlnPheGlyProLeuCysPheCysLeuAlaMetAsnTyrLeuAspArgPh
                                                                           alGlyArgArgAspAlaLeuAsnTrpIleTrpLysAlaCysGluValHis
                                                                                                                                              oSerAspAspTyrIleLysArgLeuArgSerGlyAspLeuAspLeuAsnV
|:::|||||||:::||||||||||||
                                                                                                                                                                                                                    SerGluGluIleIleMetGluMetValGluLysGluLysGlnHisLeuPr
                                                       ..CATAGAAGAGAAGCTGTTAATTGGATTTGGAAGGCTCATGTGCATTAT
                                                                                                                             AAAAGATGATTATCTTAAGAGATTGAGAATTGGGGATTTGGATTTGAAT. 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: http://www.genome.clemson.edu/orders/index.html.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hansen,C., Ronning,C. and Tanksley,S. Generation of ESTs from tomato shoot/meristem tissue Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Lycopersicon esculentum
Lycopersicon esculentum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids I; Solanales; Solanaceae; Solanum;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EST475177 tomato shoot/meristem Lycopersicon esculentum cDNA clone
                                                                                                                                                                                                                                                                                                                                                                                              Quality:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: CUGI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Lycopersicon esculentum"
/cultivar="TA496"
/db.xref="taxon:4081"
/clone="cT0F24H8"
/clone=lib="tomato shoot/meristem"
/tissue_type="shoot/meristem"
/dev_stagc="developing shoots from 4-6wks ol
/lab_host="SOLR"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="Vector: pBluescript SK(-); Site_1: EcoR1; Site_2: Xho1; Small expanding leaves from the growing tip were taken from greenhouse plants (4-6wks old TA496). Tissue was immediately frozen in liquid nitrogen."

89 c 158 g 225 t
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Gaps: 5
Percent Identity: 51.923
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BE611087
AW671293
BG595229
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7 sq75b01.yl Gm-c1048
3 LG1_333_G08.bl_A002
9 EST493907 CSTS Sola
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REFERENCE
AUTHORS
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LOCUS AW507921
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TTTGACTACAAAAGTGGTGAAGAACAGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .....CCTCAAACTCCAATGGGGGTGTTGGAA.....
                                                                                                                                                                                                                                                                                                                                      AW507921 631 bp mRNA EST 18-JUL-2000 si47a06.yl Gm-r1030 Glycine max cDNA clone GENOME SYSTEMS CLONE ID: Gm-r1030-2027 5' similar to TR:P93103 P93103 CYCLIN-D LIKE PROTEIN.
Shoemaker, R., Keim, P., Vodkin, L., Erpelding, J., Coryell, V., A., Bolla, B., Marra, M., Hillier, L., Kucaba, T., Martin, J., I. Wylie, T., Underwood, K., Steptoe, M., Theising, B., Allen, M., I. Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., R., Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., N., Ra, Waterston, R. and Wilson, R.
                                                                                                                                                     Glycine max
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids I; Fabales; Fabaceae; Papillonoideae; Phaseoleae;
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alignment_block: US-09-530-209A-2 \times AW507921
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JOURNAL
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                                                                                        167 uLeuValLeuAsnLysLeuLysTrpArgLeuArgAlaIleThrProCysS
                                                                                                                                                                                                                                                                                                                                                134 laAlaLysIleGluGluThrGluValProMetLeuIleAspLeuGlnVal
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CTATCTATAAATTACTTGGACCGATTCCTCTTTGCATATGAATTACCGAA
                                                                                                                                                                              GGTGAATCGAAGTTTTTATTTGAGGCTAAAACCATACAGAGAATGGAGCT
                                                                                                                                                                                                      GlyAspProGlnPheValPheGluAlaLysSerValGlnArgMetGluLe 167
\verb|erTyrIleArgTyrPheLeuArgLysMetSerLysCysAspGlnGluPro|
                                                          TCTTGTACTAAGCACATTGAAGTGGAGAATGCAAGCAATTACTCCTTTCA 257
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Public Soybean EST Project
Public Soybean EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Insert Length: 1012 Std Error: 0.00 High quality sequence stop: 445. Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tel: 314 286 1800
Fax: 314 286 1810
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        info@genomesystems.com_web_site: www.genomesystems.com
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="Vector: pSPORT1; Site_1: Sal1; Site_2: Not1; This cDNA library was constructed from mRNA isolated from immature cotyledons of greenhouse grown plants (individual seed fresh weight of 100-300mg). The library was prepared using the Life Technologies pSuperScript cDNA was prepared using the Life Technologies pSuperScript cDNA library construction kit. Complementary DNA was synthesized from mRNA using a poly(dT) sequence with a synthesized from mRNA using a poly(dT) sequence with a to the blunt-ended cDNA fragments followed by Not1 the blunt-ended cDNA fragments followed by Not1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            digestion. The cDNA fragments were directionally cloned into the NotI-SalI restriction site of the pSPORTI vector. The ligated cDNA fragments were transformed into E. coll ElectroMax DH10B host cells. This library was constructed by Dr. Lila Vodkin and Dr. Anu Khanna. Note that Gm-r1030 is a re-rack of Gm-c1007."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               495.00
3.278
78.646
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/clone_lib="Gm-r1030"
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/db_xref="taxon:3847"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /lab_host="DH10B"
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VERSION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GGAGAGACTATTGAA......GTGTGTTCAAATGATCCGAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     erPheSerProLeuPheSerLeuLeuGlnLysGluArgValLysLysIle
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WHE1101_A09_A17ZS Wheat etiolated seedling root normalized
WHE1101_Town Aestivum CDNA clone WHE1101_A09_A17, mRNA
                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Olin Anderson
US Department of Agriculture, Agriculture Research
West Area, Western Regional Research Center
800 Buchanan Street, Albany, CA 94710, USA
Tel: 5105595773
Fax: 5105595818
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Triticeae; Triticum.

1 (bases 1 to 621)

Anderson,O.D., Chao,S., Choi,D.W., Close,T.J., Fenton,R.D., Han Anderson,O.D., Chao,S., Lazo,G.R., Miller,R., Nguyen,H.T., P.S., Hsia,C.C., Kang,Y., Lazo,G.R., Miller,R., Nguyen,H.T., Rausch,C.J., Seaton,C.L., Tong,J.C. and Zhang,D.

The structure and function of the expressed portion of the wheat genomes - Normalized root cDNA library
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Triticum aestivum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooldeae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         sequence.
BE442681
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EST.
                                                                                                                                                                                                                                                                                                                         quality sequence with phred score less than Seq primer: Stratagene SK primer.
                                                                                                                                                                                                                                                                                                                                              Sequence have been trimmed to remove vector sequence and low quality sequence with phred score less than 20
                                                                                                                                                                                                                                                                                                                                                                                          Email: oandersn@pw.usda.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             bread wheat
/tissue_type="Root"
/dev_stage="Five day old etiolated seedling"
/lab_host-"E. coli DH10B"
/note-"Vector: Lambda Uni-ZAP XR, excised phagemid
pBluescript SK; Site_1: EcoRI; Site_2: XhoI; Seeds were
surface-sterilized, germinated and grown aseptically in
                                                                                                                                                                               /cultivar="Chinese Spring"
/db_xref="taxon:4565"
/clone="WHEII01_A09_A17"
                                                                                                                                              Library
                                                                                                                                                               /clone_lib="Wheat etiolated seedling root normalized
                                                                                                                                                                                                                                /organism="Triticum aestivum"
/cultivar="Chinese Spring"
                                                                                                                                                                                                                                                                                                    Location/Qualifiers
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the dark at room temperature on filter paper with water, nystatin and cefotaxime in covered crystallization dishes, Roots were harvested. The tissue, total RNA, and poly(A) RNA were prepared, a cDNA library was made in the TJ Close lab (Choi, Close, Fenton) at the University of California, Riverside. The cDNA clones were in vivo excised to give pBluescript phagemids before normalization was carried out. The mass excision of phagemid library and normalization were done in HT Nguyen lab by D. Zhang at Texas Tech University. Normalization protocol used was that of Soares. Plasmid DNA preparations and DNA sequencing were performed in the OD Anderson lab (all other authors)."
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alignment_block:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 201 AAAAAGGATGGAGCTTTTGGTGCTCAGCACCTTAAAATGGAGGATGCAAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               251 CTGTTACTGCTTGCTCATTTATTGACTACTTCCTGCGCAAATTCAATGAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   laAlaAlaAlaValAlaLeuSerValSerGlyGluLeuGlnArgValHis 245
                                                                                                                                                                                                                                                                                                                                                                    eAlaSerThrThrLysGlyIleAspPheLeuGluPheArgProSerGluA 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GTCGACCTGCAGGTGGTTGAGGCAAATTCTGCGTTCGAGGGGAAGACCAT
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                                                                      AGTGTTAAGATGCTACGAATTGATTCAAGACAAGATAGCAATGGGAACCA 541
                                                                                                                                                          GTCGAGCGGGCTACAACTACTTGCAAGTTC....ATAAACAAGGAGCG
                                                                                                                                                                                                    PheAspAsnSerSerPheSerProLeuPheSerLeuLeuGlnLysGluAr 262
                                                                                                                                                                                                                                                   TTGCTGCAAGTGTCGCACTTGCCGCATTTGGGGAGCGCAATACTTCAGTA 447
                                                                                                                                                                                                                                                                                                                                            CCTGAGCACAGCTAAAGGAGCTGATTTTTGGTGTTCAGACCTTCAGAGA
                                                                                                                                                                                                                                                                                                                                                                                                                                      CATGAC...GCGCCCTCCATGCTCGCATTCTCCCGCTCGACCGACCTCAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CTTGCTTGTCCCTCGCTTCAAAGATGGAGGAGACCTATGTGCCGCTCCCC 150
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SerAspGlySerAspLeuCysSer.....
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US-09-530-209A-2 x BI306295/rev
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Ratio:
Percent Similarity:
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                                                                                                                                                                           596 GACTCCGATGAGTTCGTGGCGTTGTTGGTGGAGAAGGAGATGGATCATCA
                                        75
                                                                                                                              58 uProSerAspAspTyrIleLysArgLeuArgSerGlyAspLeuAspLeuA
                                                                                                                                                                                                      42 GluSerGluGluIleIleMetGluMetValGluLysGluLysGlnHisLe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AsnGlyValLeuGluValSerAlaCys 291
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                      snValGlyArgArgAspAlaLeuAsnTrpIleTrpLysAlaCysGluVal 91
CT...TGGAGGAAAGATGCCATTGATTGGATTTGCAAGGTCCATTCCTAC 450
                                                                                       GCCTCAGCGGGGTATCTGGAGAAGCTGGAGCTCGGTGGATTGGAGTGTT
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1 (bases 1 to 790)

1 (bases 1 to 790)

1 (Pases 1 to 790)

1 (Pases 1 to 790)
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Oryza sativa
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BI306295
BI306295.1 GI:14981617
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NL_4_B12 Drought stress (leaf) Oryza sativa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: arjulsl@uohyd.ernet.in:
Insert Length: 790 Std Error:
Plate: 4 row: B column: 12
Seq primer: GTANAACGACGGCCAGTG.
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Tel: 0091-40-3010265
Fax: 0091-40-3010145
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Oryza sativa"
/cultivar="Nagina 22 (indica sub sp)"
/db_xref="taxon:4530"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /clone="NL_4_Bl2"
/clone="NL_4_Bl2"
/clone=lib="Drought stress (leaf)"
/clone_lib="Drought stress (leaf)"
/clone="Drought re leaf tissue"
/tissue_type="Botire leaf tissue"
/dev_stage="35 day-old seedlings"
/note="Organ: Leaf; Vector: T7T3Pac; ESTs from normalized leaf cDNA Library from drought stressed seedlings "
239 c 179 g 150 t
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TACAACTTTGGACCACTCAGCCTTTACCTCGCAGTGAACTACCTGGATAG 400
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 rLeuGlnValIleAlaSerThrThrLysGlyIleAspPheLeuGluPheA 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAGTTCAATGAA..
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GTCCCTCTTCCCATGGACCTTCAGGTTTTTGATGCGGAATATGTGTTTGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EST486909 MHAM Medicago truncatula/Glomus versiforme mixed library cDNA clone pMHAM-22A23 5' end, mRNA sequence.
                                                                                                                                                                         Fax: Jou Janarison@noble.org
Email: mjharrison@noble.org
Noble EST name: N380619e TIGR sequence name: MTDCA12TK More
information is available at: http://www.medicago.org
information is available at: http://www.medicago.org
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1 (bases 1 to 809)
Harrison, M.J., Liu, J., Town, C.D.,
                                                                                                                                                                                                                                                                                        2510 Sam Noble Parkway, Ardmore, OK 73401
Tel: 580-223-5810
                                                                                                                                                                                                                                                                                                                                                                      Contact: Harrison M.J.
                                                                                                                                                                                                                                                                                                                                                                                           Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                 Glomus versiforme, 2001
                                                                                                                                                                                                                                                                                                                                                                                                                                    ESTs from roots of Medicago
                                                                                                                                                                                                                                                                                                                                                                                                                                                       and Fraser, C.M.
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                                                                                                                                                                                                                                                                                                                                    The Samuel Roberts Noble Foundation
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                                                                                                                                                                   /cultivar="Medicago truncatula genotype
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/tissue_type="roots colonized with Glomus versiforme"
                       /clone_lib="MHAM"
                                                                                                                        /organism="Medicago truncatula/Glomus versiforme mixed
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180 leThrProCysSerTyrIleArgTyrPheLeuArgLysMetSerLysCys
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                                                                        nArgMetGluLeuLeuValLeuAsnLysLeuLysTrpArgLeuArgAlaI 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ACCESSION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ArgValHisPheAspAsn 248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            uGlnValIleAlaSerThrThrLysGlyIleAspPheLeuGluPheArgP
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ESTs from roots of Medicago truncatula 72 h after Rhizobium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Medicago truncatula
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids I; Fabales; Fabaceae; Papilionoldeae; Trifolieae;
                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: kate@mail.bio.tamu.edu
M394459e TIGR sequence name: MTECJ46TK More
available at: www.medicago.org
Seq primer: SKmod (CTA gAA CTA gtg gAT CC).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Inoculation, 2001
Unpublished (2001)
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barrel medic.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           College Station, Tx 77843-3258, Tel: 409 845 7707
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: VandenBosch K
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BG646052.1 GI:13781164
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Texas A&M University
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Department of Biology
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                     195
              Note="Vector: pBluescript SK -: Site_1: EcoRI; Site_2: XhOI; CDNA was prepared from polyA+ enriched RNA. The cDNJ was directionally ligated into the Unizap XR vector from Stratagene and packaged using Gigapack III Gold packaging extracts. Plasmids containing cDNA inserts were exclsed from the recombinant lambda-Zap phage using Ex-assist helper phage and propagated in XLOLR cells."
                                                                                                                                                                                                                    /tissue_type="Seedling roots"
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meliloti"
                                                                                                                                                                                             /lab_host="E. coli strain XLOLR"
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/clone_lib="KV3"
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                                                                                                                                                                                                                                                                                                                                                     /organism="Medicago truncatula"
/cultivar="genotype A17"
                                                                                                                                                                                                                                                                                                                                                                                                                      ocation/Qualifiers
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                                                                                                                                                     CDNA
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alignment_scores:

Quality:

426.50

Length:

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alignment_block:
US-09-530-209A-2 x BG646052
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 222 GATTGCTGTTTTCATCGAGCACGAGTTCAAGTTTGTTCCTGGTTTCGACT 271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 125
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                                                                                                                                                                                                                                                                                                                                                                                                                       163 lnArgMetGluLeuLeuValLeuAsnLysLeuLysTrpArgLeuArgAla 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    519
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           146
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     96 oLeuCysPheCysLeuAlaMetAsnTyrLeuAspArgPheLeuSerValH 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     80 AspAlaLeuAsnTrpIleTrpLysAlaCysGluValHisGlnPheGlyPr 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 84 CGACTGCGAGCTCCTCTGCGGGGAG.....GACTCGTCGGAGGTCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 MetAlaGluGluAsnLeu.....
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .GluLeuSerLeuCysThrGluSerAsnValAspAspGluGlyMetI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GAAGCCATTGCATGGATTCTCAAGGTACATGAGTATTATGGATTTCAGCC 368
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TCATCGCAGTTGCCGTCGTCGTCATTATTTGCCGAGGAAGAGGAGGAGTC 221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ......IleProGlnMetGlyPheSerGlnSerGluSerGluGluIl 46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TCACCGGAGATTTACCG...GAATGCTCCTCCGACCTGGATTCATCATCA 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        leValAspGluThrProIleGluIleSer.......
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   yrīleLysArgLeuArgSerGlyAspLeuAspLeuAsnValGlyArgArg 79
                                                                                                                                                                                                                                                                                                                                       IleThrProCysSerTyrIleArgTyrPheLeuArgLysMetSerLysCy
                                                                                                                                                                                                                                                                                                                                                                                      TTAGAATGGAGCTGCTTCTTGTTCTGACTATTTTGGATTGGAGGCTGAGATCA 618
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CysLeuSerLeuAlaAlaLysIleGluGluThrGluValProMetLeuIl 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  isAspLeuProSerGlyLysGlyTrpIleLeuGlnLeuLeuAlaValAla 129
                                                                                                                                    euGlnValIleAlaSerThrThrLysGlyIleAspPheLeuGluPheArg
                                                                                                                                                                                                                    CAAGCTAGATTCAACTGGAACTTTCACCCACTTCATAATTTCACGTGCTA 703
                                                                                                                                                                                                                                                         sAspGlnGluProSerAsnThr.....LeuIleSerArgSerL 209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AGACTTTCAGATTGAAGGTGCCAAATACATATTTCAACCAAGGACGATTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         eAspLeuGlnValGlyAspProGlnPheValPheGluAlaLysSerValG 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TGTTTGTCTTTAGCAGCAAAGATGGAGGAACCACTGGTTCCTTCTCTCTT
                                                 CCATCATGCATTGCTGCAGCTGCCATACTCTCTGCAGCTAATGAAATT
                                                                                    ProSerGluAlaAlaAlaAlaValAlaLeuSerValSerGlyGluLeu 241
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Percent Identity: 37.970
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seq_name:

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LOCUS BG645553
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US-09-530-209A-2 x BG645553
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                                         34 ProGlnMetGlyPheSerGlnSerGluSerGluGluIleIleMetGluMe
                                                                                     54 ATTTACCGGAATGCTCCTCCGACCTGGATTCATCATCATCATCGCAGTTG
                                                                                                                                                                            4 GACTGCGAGCTCCTCTGCGGGGAGGACCTCGTCGGAGGTCCTCACCGGAG
                                                                                                                                                                                                                      7 GluLeuSerLeuLeuCysThrGluSerAsnValAspAsp......
....GluGlyMetIleVal.Asp...GluThrProIleGluIleSerIle
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BG645553.1 GI:13780665
EST.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: kate@mail.bio.tamu.edu
M393960e TICR sequence name: MTECC60TK More information
available at: www.medicago.org
Seq primer: SKmod (CTA gAA CTA gtg gAT CC).
Location/Qualifiers
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Unpublished (2001)
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ESTs from roots of Medicago truncátula 72 h after Rhizobium
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
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Texas A&M University
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: VandenBosch K
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note-"vector: phluescript SK -; Site_1: EcoRI; Site_2: XhoI; cDNA was prepared from polyA+ enriched RNA. The cDNA was directionally ligated into the Unizap XR vector from Stratagene and packaged using Gigapack III Gold packaging extracts. Plasmids containing cDNA inserts were excised from the recombinant lambda-Zap phage using Ex-assist helper phage and propagated in XLOLR cells."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /tissue_type="Seedling roots"
/dev_stage="3 days post-inoculation with Sinorhizobium
meliloti"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Medicago truncatula"
|cullivar="genotype A17"
|db_xref="taxon:3880"
|clone="pKV3-46J23"
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68.775
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                                                                                                                           AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      213 laSerThrThrLysGlyIleAspPheLeuGluPheArgProSerGluAla 229
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             351 AATCAAATGGATGGCCACTGCAACTTTTATCTGTTGCATGTTTGTCTTTA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                251 TGGATTCTCAAGGTACATGAGTATTATGGATTTCAGCCGTTAACGGCGTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               204 TCCAATCTCGCTCTCGAATCCAGCACC...AGAGAAGAAGCCATTGCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                154 CATCGAGCACGAGTTCAAGTTTGTTCCTGGTTTCGACTACGTCTCAAGAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   euArgSerGlyAspLeuAspLeuAsnValGlyArgArgAspAlaLeuAsn 83
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                                                                                                                                                                                                                                                                                                                                                                                                                                     TGTTAAT 742
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Glomus versiforme, 2001
Unpublished (2001)
Contact: Harrison M.J.
Plant Biology Division
                                                                                                                                                                                                                                                                   BG585934 834 bp mRNA EST 11-APR-20
EST487699 MHAM Medicago truncatula/Glomus versiforme mixed
library cDNA clone pMHAM-31L19 5' end, mRNA sequence.
BG585934
                                                                                                                                          Medicago truncatula/Glomus versiforme mixed Medicago truncatula/Glomus versiforme mixed Eukaryota; mixed EST libraries.

1 (bases 1 to 834)
                                                                                                                                                                                                                                 EST
                                                                                ESTs from roots of Medicago
                                                                                                                         Harrison, M.J., Liu, J., Town, C.D., Van Aken, S., Utterback, T.,
                                                                                                                                                                                                                                                  BG585934.1 GI:13600998
                                                                                                        Fraser, C.M.
                                                                                  truncatula after
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                                                           317 GAAGCCATTGCATGGATTCTCAAGGTACATGAGTATTATGGATTTCAGCC
                                                                                                                                                                                                                                                                                            220 GATTGCTGTTTTCATCGAGCACGAGTTCAAGTTTGTTCCTGGTTTCGACT
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oLeuCysPheCysLeuAlaMetAsnTyrLeuAspArgPheLeuSerValH 113
                                                                                                              AspAlaLeuAsnTrpIleTrpLysAlaCysGluValHisGlnPheGlyPr 96
                                                                                                                                                                          ACGTCTCAAGATTCCAATCTCGCTCTCTCGAATCCAGCACC...AGAGAA 316
                                                                                                                                                                                                                                yrIleLysArgLeuArgSerGlyAspLeuAspLeuAsnValGlyArgArg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ......IleProGlnMetGlyPheSerGlnSerGluSerGluGluIl 46
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Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /tissue_type="roots colonized with Glomus versiforme"
/dev_stage="Roots harvested at 10, 17, 22, 31 and 38 days
post-inoculation with Glomus versiforme. The library was
made from a mixture of RNA from each of these stages."
/lab_host="E. coli strain XLOLR"
/note="vector: pBluescript SK: Site_1: EcoRI; Site_2:
XhoI; cDNA was prepared from polyA+ enriched RNA from
roots harvested at 10, 17, 22, 31 and 38 days
post-inoculation with Glomus versiforme. The cDNA was
post-inoculation with Glomus versiforme The cDNA was
directionally ligated into the Unizap XR vector from
Stratagene and packaged using Gigapack III Gold packaging
extracts. Plasmids containing cDNA inserts were excised
from the recombinant lambda-Zap phage using Ex-assist
helper phage and propagated in XLOLR cells."

98 a 205 c 176 g 255 t
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65.789
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/db_xref="taxon:119092"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          gb_est1:BE642779
                                                                                                                                                                                                         Emmail: sroux@uts.cc.utexas.edu
Plate: Cri2_6 row: P column.
Seq primer: SPF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Cri2_6_P20_SP6 Ceratopteris Spore Library Ceratopteris richardii ecDNA clone Cri2_6_P20 5', mRNA sequence.
                                                                                                                                                                                                                                                             Section of Molecular Cell and Developmental Biology University of Texas Biology Building, Room 16, Austin, TX 78712, USA Tel: 512 471 4238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ceratopteris richardii.
                                                                                                                                                                                                                                                                                                                                                      Contact: Roux SJ
                                                                                                                                                                                                                                                                                                                                                                                       Chatterjee, A., San Miguel, P., Stout, S.C., Banks, J. and Roux, S.J. Expressed sequence tags of cDNA clones from a C. richardii library
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EST
                                                                                                                                                                                                                                                                                                                                                                          Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                        Filicophyta; Filicopsida;
1 (bases 1 to 813)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Viridiplantae;
                                                /clone="Cri2_6_p20"
/clone_lib="Ceratopteris Spore Library"
/tissue_type="Gametophyte"
/cell_type="Spore"
                                                                                                                      /organism="Ceratopteris richardii"
/cultivar="Brogn"
/db_xref="taxon:49495"
/dev_stage="20 hours after germination initiation"
/note="Vector: pCMVSPORT6; EST sequence from cDNA
cDNA library constructed from mRNA isolated from
                                                                                                                                                                                              Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                            Streptophyta; Embryophyta; Tracheophyta; Filicales; Pteridaceae; Ceratopteris.
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GTGGCATGTATCTCATTGGCTGCAAAAATGGAAGAAGTGGAGGTGCCGTT 209
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ysThrHisAspSerSerSerSer 303
                                            TAGCAGCCCTATCGGAGTGCTTGATGCTTCATTTAGTTGTGACAGTGGAA
                                                                                                                                                                          {\tt LysLysIleGlyGluMetIleGluSerAspGlySerAspLeuCysSer..}
                                                                                                                                                                                                                        TGCAAGATACATGTGAAAGATGCTTTACCCTGCTCAGAGATGTATCAA 603
                                                                                                                                                                                                                                                                                                                 GGAACTTACTAAACTTAAGGGGAGTTTATTCTCTGTAATCCCGGCACAGC
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TTATTTTGTGCGCTATTCAGGAGCTTAAATTTCTCTCTTTTCCGGCCATCT 453
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                                                                                                                                  TTGTCACCATTTACAATGGTCAAGGATGAAAATTATGTTTTGTCAGCACC
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KEYWORDS
alignment_block:
US-09-530-209A-2 x BG726093
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JOURNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: est@watson.wustl.edu
This clone is available through: Genome Systems, Inc. 4633 World
Parkway Circle St. Louis, Missouri 63134 For further information
call: (800) 430-0030 or (314) 427-3222 FAX:(888) 919-3324 or (314)
427-3324 or contact: clones@genomesystems.com or
info@genomesystems.com web site: www.genomesystems.com
High quality sequence stop: 412.
Location/Qualifiers
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                                                                                                                                     Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA Tel: 314 286 1800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Shoemaker, R., Keim, P., Vodkin, L., Erpelding, J., Coryell, V., Khanna, A., Bolla, B., Marra, M., Hillier, L., Kucaba, T., Wartin, J., Beck, C. Wylie, T., Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers, Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurl, R., Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R., Waterston, R., and Wilson, R.
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BG726093.1 GI:14011162
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a 83 c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Glycine max"
/db_xref="taxon:3847"
/clone="cENOME SYSTEMS CLONE ID: Gm-c1055-4578"
/clone_lib="Gm-c1055"
                                                                              385.00
3.500
68.750
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/lab_host="DH10B"
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REFERENCE
AUTHORS
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ORGANISM
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KEYWORDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         105
                  source
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         aCysGluValHisGlnPheGlyProLeuCysPheCysLeuAlaMetAsnT 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CCTCAGGAAGATCACT...TGTGACCAA 474
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    alPheGluAlaLysSerValGlnArgMetGluLeuLeuValLeuAsnLys 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TGATTTTATCACTTTTGTTTGTAATTGGTTGGTTGGAGAACCTAAGTTTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CTACCCAAGATTGTCAAATATACTTTTGGGTTGGCATCTACATTTTCCTC 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GGAGATTAAAGTGCCTCCTTGTGTAGATTTACAGGTATTGTAGAATCTTA 249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        uGluThrGluValProMetLeuIleAspLeu.Gln.......
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AGTATGCAACTGTTAGCTGTAGCATGTTTGTCAATTGCTGCCAAAATGGA 199
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                                                                                                                                                                                                                                   upland cotton.

upland cotton.

Gossypium hirsutum
Gossypium hirsutum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Eukaryota; Vagnoliophyta; eudicotyledons; core eudicots;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Malvales; Malvaceae; Gossypium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   AI728767 512 bp
BNLGHill561 Six-day (
                                                                                                                                                                                                                                                                                                                                                              EST
                                                                                                                       Brookhaven National Laboratory Upton, NY 11973, USA
                                                                                                                                                                                             ESTs from developing cotton fiber Unpublished (1999)
                                                                                                          Tel: 516-344-3396
                                                                                                                                                                                  Contact: Ben Burr
                                                                                                                                                                                                                                                                                                                                                                              A1728767.1
                                                                                                                                                                                                                                                                                                                                                                                                                sequence.
                                                                                       Fax.: 516-344-3407
                                                                                                                                                              Biology Department
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                                                  il: burr@bnlux1.bnl.gov
primer: T3 Primer.
                  Location/Qualifiers
1. .512
/organism="Gossypium hirsutum"
                                                                                                                                                                                                                                                                                                                                                                              GI:5047619
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .....ValGlyAspProGlnPheV 156
                                                                                                                                                                                                                                                                                                                                                                                                                               p mRNA EST 11-JUN-19
Cotton fiber Gossypium hirsutum cDNA 5′
n D2.1 protein [Nicotiana tabacum], mRNA
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VERSION
                                                                                   seq_documentation_block:
                                                                                                                  seq_name: gb_est1:AW042725
                           ACCESSION
                                                      DEFINITION
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ORIGIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    153 GACCCTTTTTCATAAACAACAGATCAACTTATTTGATGGGTAGTTCTGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4 GluAsnLeuGluLeuSer.....LeuLeuCysThrGlu.....
                                                                                                                                                                                                                   TrpIleLeuGlnLeuLeuAlaValAlaCysLeuSerLeuAlaAlaLatysIl 137
                                                                                                                                                                                                                                                             eGluGluThrGluVal 142
                                                                                                                                                                                                    TGGACCGTGCAATTGCTTGCTTTTTTTTATCAATTGCAGCCAAAAT
                                                                                                                                             GGAGGAGACAAAAGTT 512
                                                                                                                                                                                                                                                                                                                          GGCTTCTGCTTATTACGGTTTTGGACCTTTGAGTCTTTGCCTATCCATTA
                                                                                                                                                                                                                                                                                                                                                    sAlaCysGluValHisGlnPheGlyProLeuCysPheCysLeuAlaMetA 104
                                                                                                                                                                                                                                                                                                                                                                                    GATTTGGACTTGAGTGTT...ACGAAAGAGGCTCTTGATTGGATTTGGAA 346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           luLysGlnHisLeuProSerAspAspTyrIleLysArgLeuArgSerGly
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SerAsnValAspAspGlu......GlyM 22
                              AW042725 596 bp. mRNA EST 5724F07 Pine TriplEx shoot tip library Pinus taeda ST24F07, mRNA sequence.
           AW042725.1 GI:5903254
                           AW042725
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Quality:
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3.213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /dev_stage="Six days post anthesis"
/lab_host="XI1-Blue"
/note="Vector: pBluescript II KS+"
86 c 113 g 167 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /clone_lib="Six-day Cotton fiber"
/tissue_type="immature fiber"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /cultivar="Acala Maxxa"
/db_xref="taxon:3635"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      from: 1 to: 512
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Gaps:
                                                                                                                                                                                                                                                                                                                            396
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                                                              18-SEP-1999
                                              cDNA clone
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alignment_block:
US-09-530-209A-2 x AW042725
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ORIGIN
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SOURCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AUTHORS
TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM
            202 AsnThrLeuIleSerArgSerLeuGlnValIleAlaSerThrThrLysGl 218
                                                  260 TCGTCGATTACTTCTTGCAGGGT...GGAGGGGGNANGGAGCCACCGCCG 306
                                                                                                                                                        168 uValLeuAsnLysLeuLysTrpArgLeuArgAlaIleThrProCysSerT
                                                                                                                                                                                                                                                                                                                                                                    185 yrIleArgTyrPheLeuArgLysMetSerLysCysAspGlnGluProSer
                                                                                                                                           210
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                                                                                                                                                                                                                                                                                                      110
                                                                                                                                                                                                                                                                                                              135 laLysIleGluGluThrGluValProMetLeuIleAspLeuGlnValGly 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           102 AlametAsnTyrLeuAspArgPheLeuSerValHisAspLeuProSerGI 118
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                                                                                                                                 GGTTCTGAGCACTCTGGAATGGCGGATGCTCTCTGTTACACCGTTTTCGT
                                                                                                                                                                                                            GAGCCCGACTTCCTTCGAGCCGCGTACTATCCAAAGAATGGAGCTTCT
                                                                                                                                                                                                                                                  AspProGlnPheValPheGluAlaLysSerValGlnArgMetGluLeuLe
                                                                                                                                                                                                                                                                                         TCTATAAACTATCTAGATCGGTTTCTGTCCAGGAATCCACTACCGAAAGC 59
Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Unpublished (1999)
Contact: Ross Whetten
Forest Biotechnology Group
North Carolina State University
Dept. of Forestry, NC State University, 6113 Jordan Hall, Raleigh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The Pine Gene Discovery Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Pinus; Pinus. 1 (bases 1 to 596)
Whetten,R.W., Kinlaw,C.S., Retzel,E. and Sederoff,R.R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EST. loblolly pine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: rosswhet@unity.ncsu.edu
Seq primer: 5' lambda TriplEx2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Tel: 919-515-7800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pinus taeda
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Fax: 919-515-7801
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ratio:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /Clone_lib="Plne TriplEx shoot tip library"
/lab_host="E. coli BM25.8"
/note="organ: shoot tips; Vector: Lambda TriplEx; Site_1:
Sfil (A); Site_2: Sfil (B); Shoot tips (approx. 2 cm from apex) were collected during the spring, frozen and used for mRNA isolation. The SMART-PCR method (Clontech) was used to prepare a library from 1 ug total RNA, using the Lambda TriplEx vector. Plasmid subclones in pTriplEx were recovered by cre-lox excision in E. coli strain BM25.8 and sequenced from the 5' end."

5 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     366.50
2.637
69.500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Pinus taeda"
/db_xref="taxon:3352"
/clone="ST24F07"
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Gaps: 4
Percent Identity: 41.500
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                                                                                           201
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SOURCE
ORGANISM
alignment_block:
US-09-530-209A-2 x BG597062
                                                                                                                                                                                     BASE COUNT
ORIGIN
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LOCUS BG597062
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                                                            Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                etIleGluSerAspGlySerAspLeuCysSerGlnThrProAsnGlyVal 285
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Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Cathy Ronning
The Institute for Genomic Research
For clone info: please contact Research Genetics,
Division tel 1-800-711-6195, email cdna@resgen.con
Seq primer: M13F-R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                van der Hoeven,R., Bezzerides,J., Sun,H., Cho,J., Chiemingo,A., Bougri,O., Buell,C.R., Ronning,C., Tanksley,S. and Baker,B. Generations of ESTs from sprouting potato eyes Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids I; Solanales; Solanaceae; Solanum.

1 (bases 1 to 728)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BG597062 728 bp mRNA EST 12-APR-2001 EST495740 cSTS Solanum tuberosum cDNA clone cSTS16P1 5' sequence,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        mRNA sequence.
BG597062
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           potato.
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                                                                                                                                                                                                          183
                                                                                                                                                                                                                           frozen in liquid nitrogen immediately upon removal from tubers."
                                                                                                                                                                                                                                                                /note-"Vector: pBluescript SK(-); Site_1: EcoRI; Site_2: XhOI; Various sizes of sprouting eyes (2mm to 15mm) were taken from tubers. The tubers were incubated at 26C in the dark for 2-3 weeks prior to sprouting. The eyes were
                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Solanum tuberosum"
/cultivar="Kennebec"
/db_xref="taxon:4113"
                                                        363.00
2.574
65.888
                                                                                                                                                                                                                                                                                                                                                      /tissue_type="sprouting
/dev_stage="12-14 weeks
/lab_host="SOLR"
                                                                                                                                                                                                                                                                                                                                                                                                                                      /clone="cSTS16P1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                              /clone_lib="cSTS"
                                                                                                                                                                                                          178 c
                                                              Percent
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                                                          Gaps:
Identity:
                                                                                                   Length:
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                                                                                                                                                                                                                                                                                                                                                                        eyes from tubers"
post harvest"
                                                          214
5
41.121
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KEYWORDS
SOURCE
ORGANISM
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VERSION
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LOCUS AI728683
                                                                                                                                                                                                                                                                                                                                       seq_name: gb_est1:AI728683
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          AUTHORS
TITLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        166 G.....GATTTGCCGGAATGTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    116 CTACTCTGCGGCGAAGACTCCGATACCGTTTTCTCAAACGGAGGAGGAGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                82
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              20 uGlyMetIleValAspGluThrProIleGluIleSerIleProGlnMetG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 tGluLeuLeuValLeuAsnLysLeuLysTrpArgLeuArgAlaIleThrP 182
||||:::|||||||:::||||||||
GGAGTTTCTTGTGCTGAGGATATTAGATTGGAGGCTCCGATCCATAACTC 629
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GluProSerAsnThrLeuIleSerArgSerLeuGlnValIle 212 ::: ||||||||||||||
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GlnValGlyAspProGlnPheValPheGluAlaLysSerValGlnArgMe 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GCGTATCTCGCCGTTAACTATTTCGATCGTTTTCTCTACTCGAGAAGCTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TTCACTGCT...TTCCTTATCTCAAGGGCTTCTCAGATTATC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             roCysSerTyrIleArgTyrPheLeuArgLysMetSerLysCysAspGln 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CAGGTTGAAGGTGCGAAGTATATTTGAACCAAAAACTATCCAAAGAAT 579
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GGTCTTATCGAAGATGAACGAAATTTCGTACCTGGATTTGACTATATCGA
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upland cotton.

Gossypium hirsutum

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

Rosidae; eurosids II; Malvales; Malvaceae; Gossypium.

1 (bases 1 to 562)

Blewitt,M., Matz,E.C., Davy,D.F. and Burr,B.

ESTs from developing cotton fiber
                                                                                                                                                                                                                                          BNLGHill316 Six-day Cotton fiber (to (AJ011892) cyclin D2.1 protein
                                                                                                                                                                EST
                                                                                                                                                                                  AI728683
AI728683.1
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US-09-530-209A-2 x AI728683
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                                                                                                                                                                                                                                                                                                                                    242 ....GGTTTTGCA...TTACAAAGTGATGTAATTAAGGCAATGGTTG 284
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482
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CTCTTGCTTTGATGGTGATCTTGATTTTAATGCCTTGAACGAGTTTGGGG 143
                                                                                                                                                                                                                                                                                                                                                                                                        GACCCTTTCCTTATAAACAACAGATCAACTTCTTTGATGGGTTGTCCT...
                                                                                               laMetAsnTyrLeuAspArgPheLeuSerValHisAspLeuProSerGly 118
                                                                                                                                                                                                                                                                                                                                                                   nMetGlyPheSerGlnSerGluSerGluGluIleIleMetGluMetValG 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .....AsnValAsp 18
               LysGlyTrpIleLeuGlnLeuAlaValAlaCysLeuSerLeuAlaAl 135
                                                               CCATTAACTACTTGGATCGGTTCCTATCAATGTATGATTTACCTAGAGGT
                                                                                                                                                     eTrpLysAlaCysGluValHisGlnPheGlyProLeuCysPheCysLeuA 102
                                                                                                                                                                                                   AGTGGGGATTTGGAGTTGAGC...GCCACGAGAGAGGCTATTGAATGGAT
                                                                                                                                                                                                                   SerGlyAspLeuAspLeuAsnValGlyArgAspAlaLeuAsnTrpIl 85
                                                                                                                                                                                                                                                                     AAAAAGAGATGGAGCATTTGCCTAGAGATGATTATCTTAAGAGACTGAGA
                                                                                                                                                                                                                                                                                                                                                                                                                                      AspGluGlyMetIleValAspGluThrProIleGluIleSerIleProGl 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Brookhaven National Laboratory Upton, NY 11973, USA Tel: 516-344-3396 Fax: 516-344-3407 Email: burr@bnlux1.bnl.gov Seq primer: T3 Primer.
Contact: Ben Burr
Biology Department
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/lab_host="XL1-Blue"
/lab_host="XL1-Blue"
/note="Vector: pBluescript II KS+"
/note="Vector: pBluescript II KS+"
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/cultivar="Acala Maxxa"
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3.208
64.571
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    128
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                                                                                                                                                                                                                                                             78 ArgArgAspAlaLeuAsnTrpIleTrpLysAlaCysGluValHisGlnPh
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ValAlaCysLeuSerLeuAlaAlaLysIleGluGluThrGluValProMe 144
                                                                                                                                eGlyProLeuCysPheCysLeuAlaMetAsnTyrLeuAspArgPheLeuS 111
                                                                                                                                                                                                                     AGAGATGAATCCGTTGCATGGATTCTCAAGGTACAACGCCACTATGGTTT
                                              ACTCGAGAAGCTTGCCGCAAACAAATGGCTGGCCACTTCAACTATTGTCG
                                                                                erValHisAspLeuProSerGlyLysGlyTrpIleLeuGlnLeuLeuAla 127
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BG886881
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids I; Solanales; Solanaceae; Solanum. 1 (bases 1 to 749)
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Ratio:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note-"Vector: pBluescript SK(-); Site_1: EcoRI; Site_2: /note-"Vector: pBluescript SK(-); Site_1: EcoRI; Site_2: xhoI; This library targets genes expressed in dormant tubers. This library was made from sections of dormant tuber, avoiding the buds and epidermis. Tubers were stored for one month post-harvest at 4oc. The tuber was peeled, well away from the surface. Then it was chopped into 1-2 mm cubes and immediately frozen in liquid nitrogen. This library is noted as P4 in Tanksley lab notebooks."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /tissue_type="dormant tuber"
/dev_stage="one month post-harvest"
/lab_host="SOLR"
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44	31yAspProGlnPheValPheGluAlaLysS	161
34	CCTTTTGGATCTTCAGGTTGAAGGCGCAAAGTATATTTTGAACCAAAAA 2	283
.61		177
84	CTATCCAAAGAATGGAGTTTCTTGTACTGAGGATATTAGATTGGAGGCTC	333
78	YsSerTyrIleArgTyrPheLeuArgLysMetSe	194
134	CGATCCATAACTCCGTTTAGCTTCCTCAGTTTCTTTGCGGCTAAACTTGA	383
94	rLysCysAspGlnGluProSerAsnThrLeuIleSerArgSerLeuGlnV 2	211
84		430
211	allleAlaSerThrThrLysGlyIleAspPheLeuGluPheArgProSer	227
131	ATTCAAGAAGCTAGCTTTCATGAGTATTGGCCATCA	480
228	AlaLeuSerValSerGlyGluLeuGlnArgVa	244
181	GTGCAGCTAAGGACCTT	522
244	LysG	261
523	CCAAATTTCTCTCTGTGAATGCTG	547
261	luArgValLys 264	
48	AACATGCTGAA 558	

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Post-processing: Minimum Match 0%
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REFERENCE AUTHORS TITLE JOURNAL

unclassified.

1 (bases 1 to 932)

De,A.J. and De,V.L.

CYCLIN-DEPENDENT KINASE INHIBITORS AND USES THEREOF
PATENT: WO 9914331-A 1 25-MAR-1999;
ALMEIDA JANICE DE (BE); LANDRIEU ISABELLE (BE)

LOCATION/Qualifiers

FEATURES

source

/organism="unidentified"
/db_xref="taxon:32644"
86. .715

SOURCE ORGANISM

unidentified unidentified

KEYWORDS

RESULT 1
A98054
LOCUS
DEFINITION
ACCESSION
VERSION

A98054 932 bp DNA Sequence 1 from Patent WO9914331. A98054

PAT

26-JAN-2000

ALIGNMENTS

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Direct Submission
Submitted (20-DEC-1999) Fobert
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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/translation="MAAVRRRERDVVEENGVTTTTVKRRKMEEEVDLVESRIILSPCV
QATNRGGIVARNSAGASETSVVIVRRRDSPPVEEQCQIEEEDSSVSCCSTSEEKSKRR
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/protein_id="CAB76424.1"
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

1 (bases 1 to 755)
Fowke, L. C., Wang, H. and Crosby, W.L.
Cyclin-dependent kinase inhibitors as plant growth regulators
Patent: WO 9964599-A 6 16-DEC-1999;
POWKE LARRY C (CA); WANG HONG (CA); AGRICULTURE AND AGRIFOOD CANAD
(CA); CANADA NAT RES COUNCIL (CA); CROSBY WILLIAM L (CA); UNIV
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Direct Submission

Submitted (25-JAN-2000) MIPS, at the Max-Planck-Institut fuer submitted (25-JAN-2000) MIPS, at the Max-Planck-Institut fuer Biochemie, Am Klopferspitz 18a, D-82152 Martinsried, FRG, E-mail: lemcke@mips biochem.mpg.de, mayer@mips.biochem.mpg.de Project coordinator: Marcel Salanoubat and Francis Quetier, Groupement d'Interet Public, Centre National de Sequencage - GENOSCOPE; 2 rue Gaston Cremteux, BP191, 9106 Evry Cedex, France;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     http://www.genoscope.cns.fr
On Jan 27, 2000 this sequence version replaced gi:6434247.
On Jan 27, 2000 this sequence version replaced gi:6434247.
Information on performance of analysis and a more detailed annotation of this entry and other sequences of chromosomes 3, 4 and 5 can be viewed at: http://www.mips.biochem.mpg.de/proj/thal/.
Location/Qualifiers
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2 (bases 1
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/note="355 bp LTR"
3339. .7564
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12804. .1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /translation="maavrrrerdvveengvttttvkrrkmeeevdlvesriilspcv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="similarity to cyclin-dependent kinase inhibitor (ICK1), Arabidopsis thaliana, EMBL:ATU94772_1"
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/variety="Columbia"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           join(12339. .12665,12742. .12803,12888. .13055,13125. .13197)
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complement(join(15858. .15901,16014. .16470))
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KEAELEDFFQVAEKDLRNKLLECSMKYNFDFEKDEPLGGGRYEWVKLNP"
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                                    15858. .16470
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                                                                                        complement(15858.
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                                                                                                                                                                                                                                                     'gene="T3A5.10"
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          complement(28038.
                                              complement(27723.
                                                                                    complement(27571.
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27722

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27477)

.26338)

.27200

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SLRPILLSSSSESTKGTWRELLGLKRTHVRSKKTDKVNEEVLSQDHKIISGNVAFREC
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complement(18303.
                                                                                                                                                                        /product="steroid 22-alpha-hydroxylase (DWF4)"
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TLFVLDSWQQNSIFSAQDEAKKFTFNLMAKHINSMDFGEETEGLKKEYVTFMKGVVS
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QTNIDDFPIYGHDFVSFPSRLSAPSYLNRVNKDDSASQOLPPPPASTAIWSPSPPSPQ
HPPPPPPQPDFDLNQPIFKAIHDYARKPETKPDTLIRIKESVSESGDPIQRVCYYFAE
ALSHKETESPSSSSSSSLEDFILSYKTLNDACPYSKFAHLTANQAILEATNQSNNIHI
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                                                                                                            APLNI.PGTAYHKALOSRATIIKFIERKMEERKLDIKEEDOEEEEVKTEDEAEMSKSDH
VRKQRTDDDLLGWVLKHSNI.STEQIIDLILSLLFAGHETSSVAIALAIFFIQACPKAV
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Best Local Similarity
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aatctaggataattctgtctccgtgtgtacaggcgacgaatcgcggtggaattgtggcga 248
                                                                                                                                                                                                                                                                                                       tgacgtcgtaggagattatggcggcggttaggagaagagaacgagatgtggttgaagaga
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40805. .40919,41225. .41323))
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RNP-1 signature AA179-186"
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complement(38307.
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TDRYSHRYDKMEEDDFRYERBYKRSKRSESREYVR"
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/number=6
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RESULT 5 IG6494/C LOCUS DEFINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM REFERENCE AUTHORS TITLE JOURNAL FEATURES	Qy 86 Db 1334 Qy 92 Db 1340	Qy /4 Db 1322 Qy 80 Db 1328	1310 68 1316	Qy 56 Db 1298 Qy 62 Db 1304	Qy 47 Db 1286 Qy 50 Db 1292	Qy 47 Db 1280	Qy 41: Db 1268 Qy 41: Db 1274	Qy 36 Db 1262
7218 bp DNA PAT 28-DEC 166494 7218 bp DNA PAT 28-DEC ION Sequence 14 from patent US 5670367. ION 166494 1 GI:2724471 S Unknown. NISM Unknown. Unclassified. Unclassified. 1 (bases 1 to 7218) E Recombinant fowlpox virus E Recombinant fowlpox virus Patent: US 5670367-A 14 23-SEP-1997; ES Location/Qualifiers	360 aacttttgtttgtacttccttgaggtaattaattagattcgtgtttttctcgattaata		43	69 gaagctgagttagaagatttttttcaggtggcggagaaagatctt [73	73	11	
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                                            * rhis record will be updated with the finished sequence

* note: This is a 'working draft' sequence

* This record will be updated with the finished sequence

* as soon as it is available and the accession number will
                                                                                                                                                                            on Aug 24, 1999 this sequence version replaced gi:5731886. For more information about this sequence or the Malaria Project, see http://www.sanger.ac.uk/Projects/P_falciparum. IMPORTANT: The sequence is unfinished and does not necessarily represent the correct sequence. Work on the sequence is in progress and the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PFMAL13P6 204652 bp DNA HTG
Plasmodium falciparum chromosome 13 strain
                                                                                                                              sequence may change as work continues. The sequence may be contaminated with foreign sequence from E.coli, yeast, vectorists.
                                                                                                                                                                                                                                                     CB10 1SA, UK
On Aug 24, 19
                                                                                                                                                                                                                                                                                Submitted (15-MAR-1999) P.falciparum Genome Sequencing Consortium, The Sanger Centre, Wellcome Trust Genome Campus, Hinxton, Cambridg
                                                                                                                                                                                                                                                                                                                                                                                       Plasmodium falciparum
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
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malaria parasite P.
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Flowke, L.C., Wang, H. and Crosby, W.L.
Cyclin-dependent kinase inhibitors as plant growth regulators
Patent: WO 9964599-A 3 16-DEC-1999;
FOWKE LARRY C (CA); WANG HONG (CA); AGRICULTURE AND AGRIFOOD CJ
(CA); CANADA NAT RES COUNCIL (CA); CROSBY WILLIAM L (CA); UNIV
SASKATCHEWAN TECHNOLOGIES (CA)
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/db_xref="taxon:3702"
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/chromosome="13"
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                                                                                                                                                             GAGATGCCAACGGAATCGGAAATTGAAGATTTTTTTTTGTGGAAGCTGAGAAACAACTCAAA 498
                                                                                                                                                                               gagacggtgaaggaagctgagttagaagattttttttcaggtggcggagaaagatcttcgg 616
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tgatcattgttttcaccaaagtacttattatttttcttctgtaataatctttgctttgat 796
                                  GA----AGGACGTTACGAATGGGTAAAGTTAGAGTGAAGAAGAAGAAGAAGTTTATGGTTT 606
                                                  ggtggaggaagatacgagtgggttaaattgaatccatgaagaagacgatgatgataatga 736
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Arabidopsis thaliana
Arabidopsis, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

1 (bases 1 to 856)
and Crosby, W. L.
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Arabidopsis thaliana cyclin-dependent kinase inhibitor protein
(ICKI) mRNA, complete cds.
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Wang, H., Fowke, L.C. and Crosby, W.L.
Direct Submission
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A plant cyclin-dependent kinase inhibitor
Nature 386 (6624), 451-452 (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (20-MAR-1997) Plant Biotechnology Institute, 110 Gymnasium Place, Saskatoon, SK S7N 0W9, Canada
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92 C 225 g 247 t
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                                                                                                                                                                                                                                                                                                GA---AGGACGTTACGAATGGGTAAAGTTAGAGTGAAGAAGAAGAAGAAGTTTATGGTTT
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Fowke, L.C., Wang, H. and Crosby, W.L. Cyclin-dependent kinase inhibitors as plant growth regulators Patent: WO 9964599-A 1 16-DEC-1999; FOWKE LARRY C (CA); WANG HONG (CA); AGRICULTURE AND AGRIFOOD (CA); CANADA NAT RES COUNCIL (CA); CROSBY WILLIAM L (CA); UNIVERSASKATCHEMAN TECHNOLOGIES (CA)
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1141 bp
from Patent
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Best Local Similarity
Matches 83; Conserv
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TRETMWKNNNNNNAGTWKNNNNNNAKNASAAKNYAAAAVKAAKKHWRWANKWAMRGWHAD
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                                                                                                                                                                             KWWNNYAAWYTKSSWNYTSRYYRWKTNNSWRWRSDTRSMGRANNYARABHYGYKWNTRWW
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                        tgctttgatttttcttttaacaaaatccaaatgtagatatctttctctcgaataatcaat
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                                                                                                                   BWSHTWBHBRAGAAHYWMBMMYBAKCHCMKAWYKAKKY-----AGAGGSNNNNN
                                                                                                                                              gagccacttggtggaggaagatacgagtgggttaaattgaatccatgaagaagacgatga
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Fowke, L.C., Wang, H. and Crosby, W.L.

Cyclin-dependent kinase inhibitors as plant growth regulators

Cyclin-dependent kinase inhibitors as plant growth regulators

Patent: WO 9964599-A 4 16-DEC-1999;

POWKE LARRY C (CA); WANG HONG (CA); AGRICULTURE AND AGRIFOOD

FOWKE LARRY C (CA); WANG HONG (CA); CROSBY WILLIAM L (CA); UNI
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Sequence
AX008794
malaria parasite P. falciparum.
Plasmodium falciparum
Eukaryota; Alveolata; Apicomple
                                                          complete sequence. AE001419 AE001362 AE001419.1 GI:3845
                                                                                                   AE001419 15892 bp
Plasmodium falciparum
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1 (bases 1 to 443)
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/db_xref="taxon:3702"
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 Apicomplexa; Haemosporida; Plasmodium
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (02-NOV-1998) The Institute for Genomic Medical Center Drive, Rockville, MD 20814, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Direct Submission
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Location/Qualifiers
                                                                                                          complement(8253. .9074)
/gene="PFB0820c"
                                                                                                                                                                                                                                              HKFDECDAANIMKQILSGICYLHKHNIVHRDIKPENILLENKHSLLNIKIVDFGLSSF
FSKDNKLRDRLGTAYYIAPEVLRKKYNEKCDVWSCGVILYILLCGYPPFGGQNDQDII
KKVEKGKYYFDFNDWKNISEEAKELIKLMLTYDYNKRITAKEALNSKWIKKYANNINK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /translation="mlnfillQurQGKTRFSKwyInCnEKKQKKIERDINKILINRSR
SYANIFVYENFKIVYRLYAGLYFVVCIENENELYILEFIHFMAQLLDTFFTNVCELDL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           complement(join(304. .539,666. .799,1000./gene="PFB0805c"
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/gene="PFB0805c"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /product="clathrin coat assembly protein"
/protein_id="AAC71950.1"
/db_xref="GI:3845282"
                                                      /gene="PFB0820c"
                                                                                                                                                             DEFVNMMHKICDNKSS"
                                                                                                                                                                                   LFSEERLRDAFNLFDTDKSGKITKEELANLFGLTSISEQMWNEVLGEADKNKDNMIDF
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                                                                                                                                                                                                                                                                                                                                                                                    /product="calcium-dept. protein kinase (C-term./protein_id="AAC71952.1"
/protein_id="AAC71952.1"
/db_xref="GI:3845284"
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/protein_id="AAC71951.1"
/db_xref="G1:3845283"
/translation="MDNEYKKFIEIRKRENKIGDFKITNIDINTFKKYKHKNNPTFST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LFNFHFLYYFFDNIILGGYIYEINRNIILDKINKIKKLI"
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/chromosome="2"
  /product="hypothetical protein"
                                               /note-"predicted
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AC007197.5 GI:6598710
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SQIIKMYKNKIDILNNQYNHFEVHRCKNEGKCILLIKSYFNDYLCALVNSLYIYSKDI
YSIKNENSKGEGKNKWKDKNENQNGDNIINDNIINDDNIINDNIINDDNIINDNIIYDNUDNI
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INSEKLSSVNSSYTSTEDNEFYSRKKDTLSSESEWQKCGYDAKIVRK"
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/gene="PFB0825c"
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YLNNYIDPEKNNEIYFSTNSDTISEVDETNYHEKVNNKSIEQYKNFEKDESLINHQSI
ENKRNTQNELDDNEQNILNNILKNNNHFFKEKNIYNSQNESYADSPSCSQYMSQNNSQ
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/protein_id="AAC71954.1"
/db_xref="GI;3845286"
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/db_xref="GI:3845285"
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                                      misc_feature
                                                                                                                                                                                                            source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           We thank the CSHL/WashU/ABI consortium for sequencing BAC clones F6923, F536, T17A5, and T13L16, the ESSA group for sequencing clone F13D4, and Scott Jackson, Jiming Jiang, Klaus Meyer, Eric Richards and Satoshi Tabata for helpful assistance. In addition, we would like to thank the TIGR Bioinformatics Department, especially Lixin Zhou, Hanif Khalak, Michael E. Heaney, Lily Fu, Feng Liang, Jeremy Peterson, Michael Holmes, and Delwood Richardson for software and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             their annotation. Genes with similarity to other proteins are named after the database hits. Genes without significant peptide similarity but with EST similarity are named as 'unknown' proteins. Genes without protein or EST similarity, that are predicted by two or more gene prediction programs over most of their length are annotated as 'hypothetical' proteins. Genes encoding tRNAs are predicted by tRNAscan SE (Sean Eddy,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (ftp://arthur.epm.ornl.gov/pub/xgrail), Genefinder (Phil Green, university of Washington), Genscan (Chris Burge, http://gnmic.stanford.edu/GENSCANW.html), and NetPlantGene (http://www.cbs.dtu.dk/services/NetGene2/), searches of the complete sequence against a peptide database and plant EST databases at TIGR, and manual curations based on those analyses. Annotated genes are named to indicate the level of evidence for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (09-MAR-2000) The Institute for Genomic Research, 9712 Medical Center Dr., Rockville, MD 20850, USA. On Dec 17, 1999 this sequence version replaced gi:4587677. The sequence and annotation of chromosome 2 were merged from those of the individual clones on this chromosome after removing overlaps. For detailed information, please see the TIGR web site (http://www.tigr.org/tdb/at/at.html).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Goodman,H.M., Somerville,C.R., Copenhaver,G.P., Preuss,D., Nierman,W.C., White,O., Elsen,J.A., Salzberg,S.L., Fraser,C.M. and Venter,J.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Lin,X., Kaul,S., Rounsley,S.D., Shea,T.P., Benito,M.-I., Town,C.D., Fujii,C.Y., Mason,T.M., Bowman,C.L., Barnstead,M.E., Feldblyum,T.V., Buell,C.R., Ketchum,K.A., Le,J.J., Ronning,C.M., Koo,H., Moffat,K.S., Cronin,L.A., Shen,M., VanAken,S.E., Umayam,L., Tallon,L.J., Gill,J.E., Adams,M.D., Carrera,A.J., Creasy,T.H., Goodman,H.M., Somerville,C.R., Copenhaver,G.P., Preuss,D.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              http://genome.wustl.edu/eddy/tRNAscan-SE/). Simple repeats were identified by repeatmasker (Arian Smit,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Direct Submission
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                                                                                                                                                                                                                                                                               Address all correspondence to:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          http://ftp.genome.washington.edu/RM/RepeatMasker.html). Genes are
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                                                               /db_xref="taxon:3702"
/chromosome="II"
                                                                                                                                         /organism="Arabidopsis/cultivar="Columbia"
/note="Sequence from clone F9B22"
                                                                                                                                                                                                                                     ocation/Qualifiers
                                                                                                                                                                                                                .83365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          761-768 (1999)
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                                                                                                                                                                                                                                                                                                                                                   the National Science Foundation, he US Department of Agriculture.
                                                                                                                                                                                                                                                                               at@tigr.org
                                                                                                                                                                                                                                                                                                                                               Agriculture
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               clone
                                                                                                                                                                                                                                                                                   CDS
                                                                                                                                                                                                                                                                                                                                                                                  gene
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  gene
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                                                                                                                                                                                                                                                                                                                                               complement(10550. .>12365)
/gene="At2g14100"
                                                                                                                                                                                                                                                                                                                                                                                                                                                  complement(join(10550. .11362,11445.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STSGLTFFNSTFPV"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /protein_id="AAD25849.1"
/db_xref="01:4587679"
/db_xref="01:4587679"
/translation="myageaeluvegveavaemvekvatatdemaeemaeklpeknkl
/translation="myageaeluvegveavaemvekvatatdemaeemaeklpeknkl
/kyalvlehisevaaheahliqopflhksfgfaaefyckovlskoididpicvismiln
vLeldlhysvdrgigsdnyyfdfinrsvssktfkrlklccidxdonddfysfdfphly
vLeldlhysvdrgigsdnyyfdfinrsvssktfkrlklccidxdonddfysfdfphly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             complement(join(5994..63
7229..7358,8874..9086))
/gene="At2g14090"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       complement(<5994. .>9086)
/gene="At2g14090"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          complement
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AIGSSLTYKLNQRALPTSMRFKACIYLADNGGREAGNEGRMEVYMTIMERQNDFITST
YVSLNHIFPEFLREHMYTVEYLVDVEVTSDELVFDFQLNSEKWEIGECGVLELKNHVQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CGSLERLGCSFNNPNIKCLDFTNCLKLDKEARDLIIQATARHYSILPSREVHEYITNR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SHVLERITVLELSDINIREMTPWLNRITRLRRLKLSGCGKLVSLPQLSDSLIILDAEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LPSF1GKATNLKILNLGYLSCLVELPSF1GNLHKLSELRLRGCKKLQVLPTNINLEFL
NELDLTDCILLKTFPVISTNIKRLHLRGTQIEEVPSSLRSWPRLEDLQMLYSENLSEF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SSKNLKELPDLSSATNLEVLNLNGCSSLVELPFS IGNATKLLKLELSGCSSLLELPSS IGNAINLQTIDFSHCENLVELPSSIGNATNLKELDLSCCSSLKELPSSIGNCTNLKKL HLICCSSLKELPSSIGNCTNLKKL
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QRFHYLAEKSLISINSSFYEMIDSLAQJGKEIYRKQSVREPGGROFLVDARDISEVLA
DDTAGGRSYIGIYLDLHRNDDVFNIESKAFEGMSNLQFLRVKNFGNLFBAIVCLPCLTYISRKLILDWAYSFPMTCFPSKFNPEFLVELNMWGSKLEKLMEEIQPLRNLKRMDLF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NNSTPLRDFDGLVGMGAHMEKLELLLCLDSCEVRMIGIWGPPGIGKTTIVRFLYNQLS
SSFELSIFMENIKTMHTILASSDDYSAKLILQRQFLSKILDHKDIEIPHLRVLQERLY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /translation="MDFYVFLGTVAATFFTLLGTIFYMIYGKFRVQETIITTSSSPPT
SPQSSLSCNQKHDVFPSFHGADVRKSFLSHILKEFKRKGIDTFIDNNIERSKSIGPEL
                                                                                                                                                                                                                                                                               complement(join(10727. .11362,11445. .12365))
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KHFLETMPNLEQMILYYNTPYDNDVLEVSKQLQILPRVASTKCKIQVISDNLSLSFSF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GLHHKDTIKCEEVVGCLCKYFEDIPTCLSSSPVKVVKVLKFGETFFNYDDMKKQLEQD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            YLEYSDYVAVKYPRVKFCSLVEASLNLQMTYDQCAQASYGFLVGNATDFLMGVSNVQI
LHLSDKSLEVLTFCCETIPVFNRLIHLTIKTHRHGEVGWESLPALLKNCPNLETLVFQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   7229. .7358,8874. .>9086))
/gene="At2g14090"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3674. .83164
/note="Sequence from clone T22C12"
complement(join(<5994. .6386,6474.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TFSEIDSWDNY"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GDFGKVFKKTCMGKTNAVSRKWIEALSEVATIAGEHSINWDTEAAMIEKISTDISNKL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /product="putative dis
/protein_id="AAD25848.
/db_xref="GI:6598711"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              prosite:QDOC50104)"
                                                                                                                                                                                                                                                                                                                   /note="T22C12.3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                join(1219. .1817,2190. .3300,3401. .3703,3960. .5594)
/gene="At2g14080"
                                                                                                      /protein_id="AAD25850.1"
/db_xref="GI:4587680"
                                                                                                                                                                             /product="putative cytochrome P450"
                                                                                                                                                                                                                                         /gene="At2g14100"
                                                                                                                                                                                                                                                                                                                                                                                                                  /gene="At2g14100"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="unknown protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="T22C12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IEAIKGSKIAVVLLSKDYASSSWCLNELVEIMKCRKMLDQTVMTIFYEVDPTDVKKQT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  'rpt_family="
       HDVNISSHGHPPIDECLFFGSSSFVMAPYGDYWKFMKKLMVTKLFGPQALEQSRGAR
                               SPPSLPIIGHLHLLLFDLPHKAFQKLSSKYGPLLCLRIFNVPIVLVSSASVAYEIFK
                                                                   translation="MATIVVDFQKIHFHPQILLSIFTVICIFVFFFKKPKGSRGCDLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (TA)n"
1817,2190.
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848.2"
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RESULT 14
AC016912
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                          Matches 104;
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                                                                            707
                                                                                                                                                       767
                                                                                                                                                                                                                                827
                                                                                                                                                                                                                                                                       798
                                                                                                                                                                                                                                                                                                           887- GTTAAGCGTTTATAATAAAGACATTATAAATATGATTTTTTACATAAATATTATATAAAA 828
                                                                                                             aaactataagttta 931
                                                                                                                                                                                      tcaacttttgtttgtacttccttgaggtaattaattagattcgtgtttttctcgattaat 917
                                                                                                                                                                                                                                                                     tttcttttaacaaaatccaaatgtagatatctttctctcgaataatcaataacatgtaat 857
                                                                                                                                                                                                                                                                                                                                             gatcattgttttcaccaaagtacttattatttttcttctgtaataatctttgctttgatt 797
                                                                          ATAAAATTAGTTGA
                                                                                                                                                     CAAAATATTCTTTTAACTATATCAAATACTATATAAACATTTATAACTATTTATAGAAAT 708
                                                                                                                                                                                                                                TGTCTATTAAAAAAATACATATATATATATATATATGTTCAATCGTAAACAAAAATTATA 768
                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /rpt_family="(TAAAA)n"
complement(22989. .23053)
/rpt_family="(TAAA)n"
complement(25834. .25897)
/rpt_family="POLY_A"
join(<27999. .28108,28274. .
/gene="At2g14110"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   complement(30018. .>36009)
/gene="At2g14120"
/note="T22C12.5"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ILVGDGVTLGAFRQGLTEFTQNHNSIEKNKQVWRDKYSGKPTSSETDKD"

complement(join(30018 . 30364, 30461 . 30566, 30645 . 3069)

30831 . 30977, 31067 . 31209, 31407 . 31451, 31602 . 31701,

31796 . 31909, 32117 . 32254, 32338 . 32430, 32569 . 32661,

31909 . 33102, 33505 . 335254, 32338 . 32430, 32569 . 32661,

33293 . 33402, 33505 . 33553, 33921 . 34034, 34427 . 34486,

34582 . 34560, 34447 . 35048, 35143 . 35171, 35268 . 35550,

35641 . >>36009))
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TETFALFKKLFLTQVLRRLFEILRISPFKKETLDVSRKFDELLERIIVEHEEKTDYDH
GMDLMDVLLAVYRDGKAEYKITRDHLKSLFVELILGGTDTSAQTIEWTMAKIIKKPNI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /gene="At2g14110"
/note="722C12.4; predicted by genscan"
/oin(27999. .28108,28274. .28445,28823.
/gene="At2g14110"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     complement(22545
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/rpt_family="POLY_A"
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CYVPKNTTLVVNAYAVMRDPDSWEDPDEFKPERFLASSRGKEEEREQELKYIPFGSGR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /protein_id="AAD25851.1"
/db_xref="GI:4587681"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /gene="At2g14120"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /translation="MAEEKVKDEAMQIMGMFQILPRLVVFDLDYTLWPFYCECRSKRE
#PSMYPQAKGILSALKEKGIEMAIASRSPTSDIANTFLDKLNIKPMFVAKVSKMGVTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              'note="hypothetical protein"
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                                                                          694
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                                                                                                                                                                                                                                                                                                                                                                                        0,
                                                                                                                                                                                                                                                                                                                                                                                                          Score 50;
Pred. No. 1
                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .22658)
                                                                                                                                                                                                                                                                                                                                                                                                                          DB 8; Length 83365;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .28445,28823. .>28996)
                                                                                                                                                                                                                                                                                                                                                                                      90;
                                                                                                                                                                                                                                                                                                                                                                                        Indels
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REFERENCE
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AUTHORS
TITLE
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KEYWORDS
SOURCE
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TITLE
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                                                        source
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194277
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195667
195767
197525
197625
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LOCUS
DEFINITION
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Center code: WUGSC
Web site.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Chemistry: Dye-primer ET; 33% of reads Chemistry: Dye-terminator Big Dye; 35% of reads Assembly program: Phrap; version 0.990319 Consensus quality: 198028 bases at least Q40 Consensus quality: 200051 bases at least Q30 Consensus quality: 209092 bases at least Q20 Consensus quality: 209092 bases at least Q20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (08-DEC-1999) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. MO 63108, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 213467)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Insert size: 192000; agarose-fp Insert size: 211898; sum-of-contigs Quality coverage: 7.79 in Q20 bases; agarose-fp Quality coverage: 7.63 in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequencing vector: M13; 33% Sequencing vector: plasmid;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      * NOTE: This is a 'working draft' sequence. It currently consists of 9 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown.

* This record will be updated with the finished sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Center project name: H_NH0480A06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Web site:http://genome.wustl.edu/gsc/index.shtml
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The sequence of Homo sapiens clone
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HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_ACTIVEFIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    as soon as it is available and the accession number will be preserved.
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="2"
                                                                                                     Location,
                                                                                1. .213467
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                                                                                                                            202095: gap of 0
203376: contig
203476: gap of 0
213467: contig
                                                                                                                                                                                                                  197524: contig of 1758 bp in 1
197624: gap of unknown length
199334: contig of 1710 bp in 1
199434: gap of unknown length
201995: contig of 2561 bp in 1
                                                                                                                                                                                                                                                                                                                                                                                                                                          192693: contig of 191824 bp in length 192793: gap of unknown length 194176.
                                                                                                                                                                                                                                                                                                                                                                                                   192793: gap of unknown length
194176: contig of 1383 bp in length
194276: gap of unknown length
                                                                                                                                                                                                                                                                                                                                                 195666: contig of 1390 bp in length
195766: gap of unknown length
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869: gap of unknown length
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Best Local Similarity 54.3%;
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Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; eudicotyledons; core eudicots;
Spermatophyta; Magnollophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

E 1 (bases 1 to 377)

E 1 (bases 1 to 377)

E 2 (chase 1 to 377)

E 2 (cyclin-dependent kinase inhibitors as plant growth regulators
Cyclin-dependent kinase inhibitors as plant growth regulators
PATENT C (CA); WANG HONG (CA); AGRICULTURE AND AGRIFOOD CANAD
FOWKE LARRY C (CA); WANG HONG (CA); AGRICULTURE AND AGRIFOOD CANAD
FOWKE LARRY C (CA); WANG HONG (CA); CROSBY WILLIAM L (CA); UNIV
SASKATCHEWAN TECHNOLOGIES (CA)

LOCALIC CANAD NAT RES COUNCIL (CA); CROSBY WILLIAM L (CA); UNIV
SASKATCHEWAN TECHNOLOGIES (CA)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AX008795 377 bp DNA
Sequence 5 from Patent WO9964599.
AX008795
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870. .192693
.note="assembly_name:Contig41
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192794. .194176
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47281 c 46673 g 60641 t
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199435. .201995
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195767. .197524
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194277. .195666
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                  /organism="Arabidopsis thaliana"
/db_xref="taxon:3702"
31 c 109 g 99 t
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Pred. No. 1.3;
0; Mismatches 85; Indels 0
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                                                                                              617 aataagttgttggaatgttctatgaagtataacttcgatttcgagaaagatgagccactt 676
356
TTTTTTTAACTTT 368
                   tgatcattgtttt 749
                                             GA---AGGACGTTACGAATGGGTAAAGTTAGAGTGAAGAAGAAGAAGAAGTTTATGGTTT 355
                                                            ggtggaggaagatacgagtgggttaaattgaatccatgaagaagacgatgatgatgataatga 736
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Pred. No. 1;
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Search completed: January 30, 2002, 11:55:31 Job time: 3005 sec

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Maximum Match 100%
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Maximum DB seq length: 200000000
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N_Geneseq_1101:*

1: /SIDS2/gcgdata/geneseq/geneseqn/NA1980.DAT:*
2: /SIDS2/gcgdata/geneseq/geneseqn/NA1981.DAT:*
3: /SIDS2/gcgdata/geneseq/geneseqn/NA1983.DAT:*
4: /SIDS2/gcgdata/geneseq/geneseqn/NA1983.DAT:*
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Copyright (c) 1993 - 2000 Compugen Ltd.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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No. Score Match Length DB ID No. Score Match Length DB ID Description Arabidopsis cyclin. 2 848.2 91.0 883 21 AAC45711 Arabidopsis thalia 3 840.8 90.2 886 21 AAC45711 Arabidopsis thalia 4 751.8 80.7 809 22 AAC85204 Plant D-like cycli 5 744.8 79.9 755 21 AAC29416 Arabidopsis thalia 6 223 23.9 955 21 AAC36219 C 7 116.8 12.5 936 22 AAF58252 C 8 116.8 12.5 936 22 AAF58254 Oligonucleotide D1

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AAX08523	AAZ43927	AAF62653	AAQ85027	AAT41852	AAZ33599	AAH15147	AAC59768	AAA16053	AAH13036	AAH19475	AAQ66797	AAZ10081	AAZ10091	AAQ66824	AAZ98287	AAT72882	AAA70123	AAI61373	AAA10595	AAA28122	AAV26084	AAC36958	AAZ29415	AAC47352	AAF58238	AAF58238	AAF58255	AAF58262	AAF58259	AAF58257	AAF58254	AAF58252	AAF58255
NBP46 (root lectin	Human C1D cDNA. H	DNA for 170kDa sub	Entamoeba histolyt	cDNA encoding Plas	Human breast tumou	Human cDNA sequenc	Human secreted pro	Human colon cancer	Human cDNA clone (Lactococcus lactis	AmEPV spheroidin g	Amsacta moorei ent	Amsacta moorei ent	AmEPV NPH-1 gene.		Plasmodium var-7 g	Plasmodium falcipa	Soybean 318013 reg	Gene encoding a su	Arabidopsis thalia	Tomato pest resist	Arabidopsis thalia	Arabidopsis thalia	Arabidopsis thalia	Oligonucleotide D1	Oligonucleotide D1	Oligonucleotide D1		Oligonucleotide D2		Oligonucleotide D1		

ALIGNMENTS

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RESULT
AAX25015
 Cyclin-dependent kinase inhibitor; CDK inhibitor; CKI; CDKI; FL39; plant development; transgenic plant; cell cycle; growth regulator; herbicide; ds.
                                                                                                                                              CDS
                                                                                                                                                                                                                                              05-JUL-1999 (first entry)
                                                                                                                                                                                                                                                                                   AAX25015 standard; cDNA; 932
24-DEC-1997;
16-SEP-1997;
                            16-SEP-1998;
                                                                                                          misc_feature
                                                                                                                                                                                                                              Arabidopsis cyclin-dependent kinase inhibitor FL39 cDNA clone.
                                                                                                                                                                                                                                                                 AAX25015;
                                              25-MAR-1999
                                                               WO9914331-A2
                                                                                                                                                                       Arabidopsis thaliana.
                                                                                                                           polyA_signal
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97EP-0204111.
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915..920
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Cryclin-dependent kinase (CDK) inhibitor (see AAW98179) of Arabidopsis Cryclin-dependent kinase (CDK) inhibitor (see AAW98179) of Arabidopsis Cryclin-dependent kinase (CDK) inhibitor (see AAW98179) of Arabidopsis Cryclin-dependent kinase (CDK) inhibitory and that it is system with CDC2AAt (see Cryclin as bait and a library made from an RNA mixture of A. (cryclin as bait and a library made from an RNA mixture of A. (cryclin as bait and a library made from an RNA mixture of A. (cryclin as bait and a library made from an RNA mixture of A. (cryclin as bait and a library made from an RNA mixture of A. (cryclin as bait and a library made from an RNA mixture of A. (cryclin as bait and a library made from an RNA mixture of A. (cryclin as companied in the cryclin and crycl
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    gataatgatgatcattgttttcaccaaagtacttattattttttcttctgtaataatcttt
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                                                                                                                                                                          gtctccatgagacggtgaaggtgagctgagttagaagacttttttcaggtggcggagaaag
                                                                                                                                                                                                                     acatggattcttcttcggtggctgttgaagatgtagagtctcgccgcaggttaaggaaga
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99US-0160815

99US-0160980

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99US-0161404

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05-MAR-1999

09-MAR-1999

23-MAR-1999

25-MAR-1999

26-APR-1999

16-APR-1999

16-APR-1999

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23-APR-1999

23-APR-1999

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20-APR-1999

20-APR-1999

30-APR-1999

30-APR-1999

30-APR-1999

14-MAY-1999

15-MAY-1999

16-MAY-1999

17-MAY-1999

18-MAY-1999

19-MAY-1999

21-MAY-1999

21-MA
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             Conservative
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           Score 840.8;
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83;
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08-JWN 1999
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e cyclin inhibitor gene; BRO4; dividing cells; inactivation;
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  protoplast;
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                                                                                                                                                                                                                                                                                                                                              The sequence given in AAC85204 represents a plant D1 cyclin can hibitor gene, BRO3. This sequence was isolated using a yeast two CC hybrid screen. The BRO3 protein was found to contain a seven amino CC acid sequence cyclin binding domain similar to that of BRO1, BRO2 CC and BRO4 (See also AAB47005-6). This sequence is homologous to a cc sequence present in a D-like cyclin inhibitor gene and when integrated CC at the corresponding locus, functionally inactivates plant D-like cyclin inhibitor protein expression. The BRO4 coding sequence may CC be used to produce a hyperplastic variant plant, increase the growth CC rate of a plant, or increase the proportion of dividing cells in a CC plant cell population, relative to a wild-type plant, by functionally CC gene in a plant. BRO4 is useful for increasing the proportion of CC dividing cells in a plant cell population comprising protoplast, CC seeds, root cells, meristem cells or leaf cells.
                                                                                                                                                                                                                                                            Query Match
Best Local S
Matches 753
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Functionally inactivating expression of plant D-like cyclin inhibitor gene for producing a hyperplastic variant plant, modulating the growth and/or yield of plants, and increasing the proportion of dividing cell:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              14-MAY-1999;
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                                                                                                                                                                                                                                                                                                                           Sequence
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acgacggcgagattctcctccggttgaagaacagtgtcaaatcggaagaagaagattcgtc
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                                                                                                                                                                                                                      acgacggcgagattctcctccggttgaagaacagtgtcaaatcgaagaagaagattcgtc
                                                                                                                                                        ggaggaagtggatttagtggaatctaggataattctgtctccgtgtgtacaggcgacgaa
                                                                                                                                                                                                          1; Page 39-40; 50pp; English.
                                                                                                                                                                                                                                                                         Similarity
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/product=
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99.7%;
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Pred. No. 5.4e-163;
0; Mismatches 2;
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                                                                                                                                                                                        Cyclin-Dependent kinase inhibitor; CDK; InteractiCK2; Cdc2a; D-class cyclin; CycD1; CycD2; Cyclantisense construct; tissue-specific promoter; male sterility; ds.
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                            Wang
                                                                       08-JUN-1998;
31-DEC-1998;
                                                                                                                                                                           Unidentified
                                                                                                                                                                                                                            Arabidopsis
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                                                                                                                                                                                                                            thaliana
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                                                                                                                                     Location/Qualifiers
1..531
/*tag= a
/product= "ICK2"
                                                                       98CA-2235978.
98CA-2256121.
                                                                                             99WO-CA00532
                             Crosby WL
                                                                                                                                                                                                                            CDK inhibitor,
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                                                                                                                                                                                                              Interactor of Cdc2 kinase
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ter; transgenic plant;
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Modifying plant cell development using nucleic acid encoding inhibitor of cyclin-dependent kinase, or corresponding antisense sequence, e.g. for inducing male sterility .
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The present sequence is a cDNA encoding ICK2 which inhibits A. thaliana Cyclin-Dependent kinase (CDK). Interactor of Cdc2 kinase 2 (ICK2) interacts with Cdc2a, D-class cyclins, CycDl, CycD2 and CycD3 and shares functional and sequence similarity with ICK1. Growth, morphogenesis, multiplication, enlargement, differentiation and maturation of plant cells can be modified by transforming them with nucleic acid encoding CDK inhibitor or antisense construct complementary to the inhibitor gene, operably linked to a tissue-specific promoter. The transgenic plants exhibit alteration of traits such as petals, male sterility and ability to set seeds.

Sequence BP; 229 A; 106 Ç; 187 ٠<u>.</u> 233 Ħ, 0 other;

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               ctttgctttgatttttcttttaacaaaatccaaatgtagatatctttctctcgaataatc
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99.78;
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Pred. No. 2.1e-161
0; Mismatches 2
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                               gccacttggtggaggaagatacgagtgggttaaattgaatccatgaagaagacgatgatg 729
gccacttggtggaggaagatacgagtgggttaaattgaatccatgaagaagacgatgatg
                                                                   240;
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                                                                  Conservative
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9908-0159331.
9908-0159534.
9908-0160748.
9908-0160767.
9908-0160767.
9908-0160768.
9908-0160768.
9908-0160814.
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9908-016081.
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9908-0161393.
9908-0161393.
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Pred. No. 5e-47
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RESULT 7
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                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 936 BP; 4 A; 139 C; 10 G;
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a single surface -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Page 127; 159pp; English.
                                                                                                                                                                                                                                                                             12.5%; Score 116.8; DB ilarity 6.3%; Pred. No. 1.1e-17; Conservative 459; Mismatches 35
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2000US-0190259.
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RESULT 8
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             26-JUL-2000; 2000WO-US20476.
                              01-FEB-2001
                                           WO200107665-A2
                                                                             Electron-transfer group; ETM; mismatch; genotyping;
                                                                                                                                        AAF58254 standard; DNA;
                                                          Synthetic
                                                                                             Oligonucleotide D1875
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99US-0145695
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                                                                                   aagatgagccacttggtggaggaagatacgagtgggttaaattgaatccatgaagaagac
                                                                                                                                                 agaaagatcttcggaataagttgttggaatgttctatgaagtataacttcgatttcgaga
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RESULT 9
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AC AAF58257;
AC AAF58257;
XX DF Oligonucleotide D195
XX Electron-transfer gr
KW gene expression; ss.
XX Synthetic.
XX Synthetic.
XX PN 'WO200107665-A2.
XX 'WO200107665-A2.
XX PP - 26-JUL-1999; 99US-PR - 26-JUL-1999; 99US-PR - 17-MAR-2000; 2000WO-XX
PD : 26-JUL-1999; 99US-PR - 17-MAR-2000; 2000WO-XX
PR : 26-JUL-1999; 99US-PR - 17-MAR-2000; 2000WO-XX
PD : 26-JUL-1999; 99US-PR - 17-MAR-2000; 2000WO-XX
PD : 26-JUL-1999; 99US-YX
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17-MAR-2000; 2000US-0190259.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Example 6; Page 127; 159pp; English.
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Local Similarity 6.3%;
nes 55; Conservative 45
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                                                                                                                                                                                                 %; Score 116.8; DB 22; ; Pred. No. 1.1e-17; 459; Mismatches 356;
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RESULT 10
AAF58259/c
ID AAF582
XX AAF582
XC AAF582
XC AAF582
XX DE Oligon
XX Electr
KW gene e
XX Synthe
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XX W02001
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                                                                                   Electron-transfer group;
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                                                                                   genotyping;
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17-MAR-2000;
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gtgacgatcgtgaaacagaaacgtcgtggatttacgatgatttgaataagagtgaggaat
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2000US-0190259
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Pred. No. 1.1e-17;
59; Mismatches 35
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ID AAF58262/
AC AAF5
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17-MAR-2000;
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WO200107665-A2
            Synthetic
                             Electron-transfer group;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 938 BP; 4 A; 144 C;
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17-MAR-2000; 2000US-0190259.
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                                                                                                                                                                                                                                                                                                                                                                                                                             459;
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                                                                                      The present invention relates to a composition comprising two nucleic acids each containing an electron-transfer group (ETM) having different redox potentials. The invention is used for electronic detection of nucleic acids, especially of substitutions (mismatches) and single-nucleotide polymorphisms, e.g. for genotyping, monitoring gene expression.
                                                                      Sequence
                                                                                                                                                                            Nucleic acids containing electron-transfer group, useful as labels in hybridization assays, e.g. for genotyping, allowing repeat analyses on a single surface
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                                                                                                                                                                                                                                                                                                                                                                   Synthetic.
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wene expression; ss.
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17-MAR-2000; 2000US-0190259.
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312 ttgaagaacagtgtcaaatcgaagaagaagattcgtcggtttcgtgttgttctacatcgg 371
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                                                                    4 A; 139 C; 10 G; 7 T; 776 other
                              11.9%;
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                     ; Pred. No. 2.4e-
395; Mismatches
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2.4e-16;
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RESULT 14
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17-MAR-2000;
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                                                                                                   Synthetic
                                                                                                               Electron-transfer group; ETM; mismatch; genotyping;
gene expression; ss.
                                                                                                                                   Oligonucleotide D1875
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Matches 6; Conserv
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  24-APR-2001
                      AAF58257;
                                          AAF58257 standard; DNA; 936
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                                          ВP
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                                                                                                                                                                                                                                                                                                                          Sequence 936 BP; 5 A; 142 C; 7 G; 6 T;
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Drosophila melanogaster genome survey sequence TET3 end of BAC #
BACR08K10 of RPCI-98 library from Drosophila melanogaster (fruit
              Genoscope.
Direct Submission
Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage BP 191 91006 EVRY cedex - FRANCE (E-mail : segrefégenoscope.cns.fi
                           Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.

1 (bases 1 to 1101)
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 segref@genoscope.cns.fr
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AL106896 AL108152 AL053529 AZ544590 AL436064

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T3 end of BMBAG08B2 ENTCE20TR

AL09730 AZ68933

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AL078714 Drosophil
AL108536 Drosophil
AL108537 Drosophil
AL0087377 Drosophil

Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial ECORI digestion of Drosophila DNA provided by the BDGP from the isogenic strain y2; on bw sp, the same strain used for the BDGP's P1 and EST libraries. A more detailed description of the ibrary and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.

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    Web: www.genoscope.cns.fr)
    Determination of this BAC-end sequence was collaboration with the Berkeley Drosophila

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Web: www.genoscope.cns.fr)
Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila
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Submitted (02-JUN-1999) Genoscope - Centre
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Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                 fruit fly.
                                                                                                                                                          scomorpha; Ephydroidea; (bases 1 to 1101)
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/db_xref="taxon:7227"
/clone_lib="RPCI-98"
/clone="BACR27A24"
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Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial
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Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.

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Location/Qualifiers
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/clone_lib="RPCI-98"
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AL175696.1 GSS; genome AL175696 sequence.

GI:7813753

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Drosophila melanogaster genome survey sequence TET3 end of BAC #
BACR08K10 of RPCI-98 library from Drosophila melanogaster (fruit
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AL063921
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Drosophila
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67; Conserv
Chlamydomonadaceae; (bases 1 to 702)
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                                                               Chlamydomonas reinhardtii. Chlamydomonas reinhardtii
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  - Web: www.genoscope.cns.fr)
Determination of this BAC-end sequence was carried out as potential boration with the Berkeley Drosophila Genome Project The BDGP is constructing a physical map of the Drosophila
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pl and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be
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                                                                                                                                                                                                                                                                                                      Drosophila melanogaster genome survey sequence TET3 end of BAC:
BACR48P19 of RPCI-98 library from Drosophila melanogaster (fruitily), genomic survey sequence.
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fruit fly.
                           Direct Submission
Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage
RP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fl
                                                                                                                                                                                                                                                                                                          fly), gen
AL108536
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Drosophila melanogaster genome survey sequence SP6 end of BAC
BACN37L10 of DrosBAC library from Drosophila melanogaster (fruit
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Direct Submission
BP 191 91006 EVRY cedex - FRAN-
- Web : www.genoscope.cns.fr)
Determination of this BAC-end
                                                                                                                             Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.

1 (bases 1 to 1101)
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/db_xref="taxon:7227"
/clone_lib="RPCI-98"
/clone="BACR48P19"
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  carried out
                                           segref@genoscope.cns.fr
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as part of
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collaboration with the European Drosophila Genome Project (EDGP) http://www.edgp.ebi.ac.uk - This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billaud at CEPH (Centre

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SOURCE
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                                                                                        Plasmid Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 1101)
                             Submitted (23-JUL-1999) Genoscope - Centre BP 191 91006 EVRY cedex - FRANCE (E-mail :
                                                                                                                                                                                                                                     CNS00293 1101 bp DNA GSS 26-JUL-1999
Drosophila melanogaster genome survey sequence T7 end of BAC
BACNO1G23 of DrosBAC library from Drosophila melanogaster (fr
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                                                              Direct Submission
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ilarity 38.5%;
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www.genoscope.cns.fr)
nation of this BAC-end sequence
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/plasmid="pBeloBAC11"
/db_xref="taxon:7227"
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/clone="BACN37L10"
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                              segref@genoscope.cns.fr
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Determination of this BAC-end sequence was carried out as part of a collaboration with the European Drosophila Genome Project (EDGP) - http://www.edgp.ebi.ac.uk - This Drosophila melanogaster BAC http://www.edgp.ebi.ac.uk - JAlain Billaud at CEPH (Centre d'Etude du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton and Genevieve Payan. It has been constructed in the vector
                                                                                                                                                                                                                                                                                                                                               Plasmid Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Ins
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
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Direct Submission
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/plasmid="pBeloBAC11"
/db_xref="taxon:7227"
/clone_lib="DrosBAC"
/organism="Drosophila
                                      Location/Qualifiers
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/note="end : T7"
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/plasmid="pBeloBAC11" /db_xref="taxon:7227"

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RESULT 12
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                                                                                                                                                                        - Web: www.genoscope.cns.fr)

Determination of this BAC-end sequence was carried out as part of collaboration with the European Drosophila Genome Project (EDGP) - http://www.edgp.ebi.ac.uk - This Drosophila melanogaster BAC http://www.edgp.ebi.ac.uk - This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billaud at CEPH (Centre d'Etude du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CNS017KX 1101 bp DNA
Drosophila melanogaster genome
BACN37F10 of DrosBAC library fx
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AL108171
                                                                                                                                                                                                                                                                                        Submitted (23-JUL-1999) Genoscope - Centre BP 191 91006 EVRY cedex - FRANCE (E-mail:
                                                                                                                                                                                                                                                                                                                                                          Muscomorpha; Ephydroidea; Drosophilidae; Drosophila
1 (bases 1 to 1101)
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Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
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/clone="BACN15C18"
/note="end : SP6"
a 128 c 38 g
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/note="end : 84 c
                              /clone_lib="DrosBAC"
/clone="BACN37F10"
                                                                /db_xref="taxon:7227"
                                                                              /organism="Drosophila
/plasmid="pBeloBAC11"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            fly), genom
AL106249
AL106249.1
                                                                                                                                                                                                            Web: www.genoscope.cns.fr)
Determination of this BAC-end sequence was carried out as part of a collaboration with the European Drosophila Genome Project (EDGP)-http://www.edgp.ebi.ac.uk - This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billaud at CEPH (Centre d'Etude du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton and Genevieve Payan. It has been constructed in the vector
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Plasmid Drosophila melanogaster
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                                                                                                                                                                                                                                                                                                                                                                       Submitted (23-JUL-1999) Genoscope - Centre National de Sequençage
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cms.fr
                                                                                                                                                                                                                                                                                                                                                                                                                                   Genoscope.
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Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
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                /organism="Drosophila m
/plasmid="pBeloBAC11"
/db_xref="taxon:7227"
/clone_lib="DrosBAC"
/clone="BACN15021"
/note="end : SP6"
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Query Match

. 68;

Score 51.8;

В

13;

Length 1201;

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REFERENCE
AUTHORS
TITLE
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CNS00LJT/c
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1 (bases 1 to 1101)
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/clone="BACR30P10"
/note="end : T7"
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/db_xref="taxon:7227"
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/clone="BACN37A19"
/note="end : T7"
a 147 c 153 g
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/plasmid="pBeloBAC11"
/db_xref="taxon:7227"
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                                                                                                                    tgatgataatgatgatcattgttttcaccaaagtacttattatttttcttctgtaataat 784
- Web: www.genoscope.cns.fr)
Determination of this BAC-end sequence was carried out as part of a collaboration with the European Drosophila Genome Project (EDGP)-
http://www.edgp.ebi.ac.uk - This Drosophila melanogaster BAC
library (Dros BAC) was made by Alain Billaud at CEPH (Centre
d'Etude du Polymorphisme Humain) with funding provided by a MRC
project grant. The DNA was prepared from embryos by Alain Bucheton
and Genevieve Payan. It has been constructed in the vector
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Drosophila melanogaster genome survey sequence T7 end of BAC
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Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
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                 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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Copyright (c) 1993 - 2000 Compugen Ltd.
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/cgn2_6/ptodata/2/ina/5B_COMB.seq:*
/cgn2_6/ptodata/2/ina/6B_COMB.seq:*
/cgn2_6/ptodata/2/ina/6B_COMB.seq:*
/cgn2_6/ptodata/2/ina/FCTUS_COMB.seq:*
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US-08-998-416-28
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US-08-998-416-28
US-08-998-416-36
US-08-449-043-36
US-08-449-043-36
US-08-455-244-36
US-08-455-246-36
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Sequence 14, Appl
Sequence 1, Appl
Sequence 41, Appl
Sequence 41, Appl
Sequence 1, Appl
Sequence 1, Appl
Sequence 1, Appl
Sequence 1, Appl
Sequence 4, Appl
Sequence 4, Appl
Sequence 4, Appl
Sequence 5, Appl
Sequence 5, Appl
Sequence 5, Appl
Sequence 36, Appl
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Sequence 487, App	Patent No. 5231168	Sequence 14, Appl	Sequence 1, Appli	Sequence 13, Appl	Sequence 1137, Ap	Sequence 4, Appli	Sequence 166, App	Sequence 2, Appli	Sequence 4, Appli	Sequence 186, App							

ALIGNMENTS

US-08-232-463-14/c Sequence 14, Applicat Patent No. 5670367 GENERAL INFORMATION: COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/232,463
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION UMBER: US/07/935,313
FILING DATE:
APPLICATION NUMBER: EP 91 114 300.6 INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 7218 base pair STRANDEDNESS: S
TOPOLOGY: linea:
IMMEDIATE SOURCE:
CLONE: pTZgpt-F APPLICANT: SCHETFLINGER, F.
APPLICANT: FALKNER, F. G.
TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 1800 Diagonal Road, Suite 500
CITY: Alexandria FILING DATE: 26-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 30472/114 IMMU
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)836-9300
TELEPHONE: (703)836-9300 APPLICANT: TELLETAX: (/TELEFAX: 899149 STATE: VA COUNTRY: USA ZIP: 22313-0299 nucleic acid nucleic single Application US/08232463 (703)683-4109 DORNER, linear single 'n, 14:

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US-08-947-823-1
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Best Local Similarity

Matches 27; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 1, Application US/08947823 Patent No. 6114605
                          PRILING DATE: 09-OCT-199/
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/028/.
EILING DATE: 10-OCT-1996
ATTORNEY/AGENT INFORMATION:
NAME: Bastian, Kevin L.
NAME: Bastian, Kevin L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/947,823
FILING DATE: 09-OCT-1997
CLASSIFICATION: 800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1219
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                                                                                                                                      PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US97/18802
FILING DATE: 09-OCT-1997
                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: Pest Resistance NUMBER OF SEQUENCES: 5
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                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  43
                                                                                                                                                                                                                                                                                                                                                                         CITY: San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                           MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                             COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: Townsend and Townsend and Crew LLP STREET: Two Embarcadero Center, Eighth Floor
                   REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ttagagagagatagagatctggaaggtgacgtcgtaggagattatggcggcggttaggag 102
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Yaghoobi, Jafar
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                                                                                    UMBER: US 60/028,191
10-OCT-1996
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Stephen
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                   023070-070210US
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                               Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 13,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL
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                                                                                                                                                                                                                                                                                         APPLICANT: Su, Xin-zhaun
APPLICANT: Wellems, Thomas E.
TITLE OF INVENTION: BINDING DOMAINS FROM PLASMODIUM VIVAX
TITLE OF INVENTION: AND PLASMODIUM FALCIPARUM ERYTHROCYTE BINDING PROTEINS
NUMBER OF SEQUENCES: 45
                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
COMPUTER: IBM PC com
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                                                                           COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS
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               ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES:
                                                                                                                                                                                             STREET: 620 NO., CITY: Newport Beach STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRANDEDNESS:
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                                                                                                                                                                                         COUNTRY:
                                                                                                                                                                                                                                                       ADDRESSEE:
                               CLASSIFICATION:
                                             FILING DATE:
                                                            APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          agatatotttototogaataatoaataacatgtaat-toaacttttgtttgttacttoott 880
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TTAAAGAATTCTTATGTAAACATATGTTAATATTTGTTACAGAATATGACCACTAAATTC 3265
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                                                                                                                                                                            92660
Israelsen,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Application US/08487826B
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
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                                                                                                                                                                                                                                                                                                                                                                                   Chitnis, Chetan
Miller, Louis H.
                                                                                                                                                                                                                                                                                                                                                                                                                   Sim, Kim L
                                                                                                                                                                                                                                                                                                                                                                      Peterson, David S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (415) 576-0200
15) 576-0300
                                                                                                                                            Floppy disk
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         single
                                   10-SEP-1993
N: 435
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                                                               US/08/487,826B
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Pred. No.
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                                                                                                                                                                                                                                            16th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   160;
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RESULT 4
US-07-991-867B-41
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Patent No. 547678
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 41,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
        FILING DATE: 12-DEC-1992
CLASSIFICATION: 435
PRIOR APPLICATION DATA: WO 92/14818
APPLICATION NUMBER: WO 92/14818
FILING DATE: 12-FEB-1992
PRIOR APPLICATION NUMBER: US 07/827,685
FILING DATE: 30-JAN-1992
PRIOR APPLICATION NUMBER: US 07/657,584
APPLICATION NUMBER: US 07/657,584
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: (619) 235-017
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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HYPOTHETICAL: N
ANTI-SENSE: NO
                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
ADDRESSEE: David R. Saliwanchik
STREET: 2421 N.W. 41st Street, Suite A-1
                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Moyer, Richard W.
APPLICANT: Hall, Richard L.
APPLICANT: Gruidl, Michael E.
TITLE OF INVENTION: No. 5476781el Entomopoxvirus Expression System
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REFERENCE/DOCKET NUMBER: NIT
TELECOMMUNICATION INFORMATION:
TELEPHONE; (619) 235-8550
                                                                                                                                                                 SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/991,867B
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       905 tt
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ZIP: 32606
                                                                                                                                                                                                                                                                                                                 STATE:
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19-FEB-1991
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US-08-544-332-41
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Best Local Similarity
Matches 98; Conserv
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                                                FILING DATE: 07-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 0:
FILING DATE: 19-AUG-1993
                                                                                                                                         CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                    COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES: 77
CORRESPONDENCE ADDRESS:
ADDRESSEE: Gerard H. Bencen
STREET: 2421 N.W. 41st Stree
                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Hall, Richard L.
APPLICANT: Gruidl, Michael E.
TITLE OF INVENTION: No. 5935777el Entomopoxvirus Expression System NUMBER OF SEQUENCES: 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
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                              PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                     STREET: 2422
CTTY: Gainesville
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Saliwanchik, David R. REGISTRATION NUMBER: 31,794
REFERENCE/DOCKET NUMBER: UF
                                                                                                        APPLICATION NUMBER: US 0' FILING DATE: 07-DEC-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 1689 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                   FILING DATE:
                                                                                                                                                                                                   APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                COUNTRY:
                 APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                32606
                                                                                                                                                                                                                                                                                                                                                   USA
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MBER: WO 92/14818
12-FEB-1992
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                                                                                                                                                                                                                                                                                                                                                                                                         41st Street,
                                                                                                                           US 07/991,867
                                                                     US 08/107,755
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Pred. No. 0.033;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 1;
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                                                                                                        MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
                                        PRIOR APPLICATION DATA:
                                                                                                                                                                                         MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Moyer, Richard W. APPLICANT: Hall, Richard L. APPLICANT: Gruidl, Michael E
                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES: 60
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Gruidl, Michael E. TITLE OF INVENTION: NO. 54767
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE: 19-FEB-1991 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      847 ATTAAATT 854
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APPLICATION NUMBER:
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APPLICATION NUMBER: WO 9
FTLING DATE: 12-FEB-1992
                                                           CLASSIFICATION:
                                                                           APPLICATION NUMBER: US/07/991,867B FILING DATE: 12-DEC-1992
                                                                                                                                                                                                                             COUNTRY: U
                                                                                                                                                                                                                                                                               STREET: 2421 N.W. CITY: Gainesville
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 1689 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                        ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Match 4.78;
Local Similarity 52.18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US 0 FILING DATE: 30-JAN-1992
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                                                                                                                                                                                                                                                                                                 E: David R. Saliwanchik
2421 N.W. 41st Street, Suite A-1
                                                                                                                                                                                                                                             USA
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                                                                                                                                                                                                                                                                                                                                                                        No. 5476781el Entomopoxvirus Expression System
                   WO 92/14818
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Pred. No. 0.033;
"Asmatches 90; Indels
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Patent No. 5937...
Patent No. 5937...
Patent No. 5937...
GENERAL INFORMATION:
APPLICANT: Moyer, Richard M.
APPLICANT: Hall, Richard L.
ADDLICANT: Gruidl, Michael E.
ADDLICANT: Gruidl, Michael E.
ADDLICANT: No. 5935777el Entomopoxvirus Expression System
                                                                                                                                              Sequence 1, Application US/08544332 Patent No. 5935777
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 4.7
Best Local Similarity 52.1
Matches 98; Conservative
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                                                                                                                                                                                                                                                7615 ATTAAATT 7622
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                                                                                                                                                                                                                                                                                                                   7555 ATTATTTATATATTCTTCTTTTATATTCATAACATTTGGTCTAAGTAAACCTATTAAATT 7614
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ORIGINAL SOURCE:
ORGANISM: Ams
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LENGTH: 8457 base pairs
TYPE: nucleic acid
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APPLICATION NUMBER:
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1474..2151
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2502..2987
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NUMBER OF SEQUENCES: 7

ADDRESSEE:

E: Gerard H. Bencen 2421 N.W. 41st Street, Suite A-1

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US-08-544-332-1
               Query Match
Best Local Similarity
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LENGTH: 8457 base pairs
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TELEPHONE: 904-375-8100
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APPLICATION NUMBER: US 0'
FILING DATE: 07-DEC-1992
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ORIGINAL SOURCE:
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ATTORNEY/AGENT INFORMATION:
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APPLICATION NUMBER: US 07/827,685
FILING DATE: 30-JAN-1992
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
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LOCATION:
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OPERATING SYSTEM: PC-DOS/MS-DOS
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FILING DATE: 19-AUG-1993
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STRANDEDNESS: odouble
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3080..6091
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4.7%; Score 44; DB 2; Length 8457; 52.1%; Pred. No. 0.054; Itive 0; Mismatches 90; Indels
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Best Local Similarity
Watches 85; Conserve
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                                                                                                     Sequence 4, Application US/08569214 Patent No. 6165469
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APPLICANT: ENDEGE, WILSON O.,
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Patent No. 6262334
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EARLIER FILING DATE: 1999-06-08
EARLIER APPLICATION NUMBER: 60/117,393
EARLIER FILING DATE: 1999-01-27
EARLIER APPLICATION NUMBER: 60/098,639
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                                                                                    GENERAL INFORMATION:
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LOCATION: (1)...(471)
OTHER INFORMATION: n = A,T,C
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ORGANISM: Homo
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APPLICANT: MANN, BARBARA J.
APPLICANY: PETRI, WILLIAM A.
TITLE OF INVENTION: RECOMBIN
TITLE OF INVENTION: SUBUNIT
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FILING DATE: 1999-08-30
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RECOMBINANT ENTAMOEBA HISTOLYTICA LECTIN SUBUNIT PEPTIDES AND REAGANTS SPECIFIC FOR MEMBERS OF
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 Mismatches

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 41.8; DB 4;
Pred. No. 0.077;
Pred. No. 72;
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THE

TITLE OF INVENTION: 1:
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS

170 KD SUBUNIT MULTIGENE FAMILY

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US-08-937-236-4/c
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Best Local Similarity 51.6%;
Matches 95; Conservative
                                                                                                          Sequence 4, Application US/08937236
Patent No. 6187310
                                                             GENERAL INFORMATION:
APPLICANT: MANN, I
APPLICANT: PETRI,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/
FILING DATE: 17-JUN-1994
ATTORNEY/AGENT INFORMATION:
NAME: MURASHIGE, KATE H.
REGISTRATION NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 9148
TELECOMMUNICATION INFORMATION:
TELECHONE: (202) 887-1500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ZIP: 200006-1812
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: MANN, BARBARA J.
APPLICANT: PETRI, WILLIAM A.
APPLICANT: DODSON, JAMES M.
TITLE OF INVENTION: RECOMBINANT ENTAMOEBA HISTOLYTICA LECTIN
TITLE OF INVENTION: SUBUNIT PEPTIDES AND REAGANTS SPECIFIC FOR MEMBERS
TITLE OF INVENTION: 170 KD SUBUNIT MULTIGENE FAMILY
                                                                                                                                                                                                                                                                          3961 TCAATTCTCTTAATTATTGTTCTTATCCATTGAATGTTGCTGCATTAGTTGCTTCATTAT 3902
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                                                                                                                                                                                                             3901 CTGC 3898
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TOPOLOGY: li
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TELEX: 90-4030
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EDNESS: single
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61..3936
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US-08-937-236-4
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TELEFAX: (202) 887-0763
TELEFAX: (202) 887-0763
TELEFAX: 90-4030
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 4090 base pairs
TYPE: nucleic acid
TYPE: nucleic acid
STRANDENNESS: single
                                                                                                                                      Sequence 288, Application US/08998416 Patent No. 6239264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
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Best Local Similarity
                                                                                                                          GENERAL INFORMATION:
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CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER: 29
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 887-1500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: 08/569,214
FILING DATE: 16 SEPTEMBER 1997
ATTORNEY/AGENT INFORMATION:
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PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FEATURE:
                                                                                                                                                                                                                                                                                                                     3961 TCAATTCTCTTAATTATTGTTCTTATCCATTGAATGTTGCTGCATTAGTTGCTTCATTAT 3902
                                                                                                                                                                                                                                                 3901 CTGC 3898
                APPLICANT:
                                   APPLICANT:
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APPLICANT:
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APPLICANT:
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                                                                                                                                                                                                                                                                                   896 attc 899
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STREET: 2000 PENI
CITY: WASHINGTON
STATE: DC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                           ATTGTTTATCACTCAATTTATTCTTCTTTTTATTTTTAATCTAAAAACATAAAATGTTAT 3962
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            95;
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2000 PENNSYLVANIA AVENUE N.W., STE. 5500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
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61..3936
                Wendland, Jurgen
Knechtle, Philipp
                                                                  Philippsen, Peter
Pohlmann, Rainer
Steiner, Sabine
Rebischung, Corinne
                                                 Mohr, Christine
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Pred. No. 0.17;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                89;
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RESULT 12
US-09-056-075-1/c
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                                                                                                                Sequence 1, Application US/09056075 Patent No. 5955368
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 4.3%;
Best Local Similarity 51.1%;
Matches 119; Conservative
                                                                                                GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: 919-541-8689
INFORMATION FOR SEQ ID NO:
               APPLICANT: Johnson,
APPLICANT: Bradshaw,
APPLICANT: Rood, Jul
TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
LENGTH: 837 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: CH 0016/97
FILING DATE: 31-DEC-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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CORRESPONDENCE ADDRESS:
 NUMBER OF SEQUENCES:
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                                                                                                                                                                                                                                    864 tttgtttgtacttccttgaggtaattaattagattcgtgtttttctcgattaa 916
                                                                                                                                                                                                                                                                                                                                                                                                                                     685 aagatacgagtgggttaaattgaatccatgaagacgatgatgatgataatgatgatcatt 744
                                                                                                                                                                                                                  805 taac-aaaatccaaatgtagatatctttctctcgaataatcaataacatgtaattcaact 863
                                                                                                                                                                                                                                                                                                                                                  STRANDEDNESS: single TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Meigs, J. Timothy REGISTRATION NUMBER: 38 REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US/08/998,416 FILING DATE: 24-DEC-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY: U
ZIP: 27709
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEPHONE:
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  Research Triangle Park
: No. 6239264th Carolina
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                                                              Bradshaw, Marite
                                                                                 Johnson, Eric A.
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                                                Julian
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AND USES THEREOF
Expression System for Clostridium Species
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US-08-231-342-5/c
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                                                                                                                                                                   Sequence 5, Application US/08231342 Patent No. 5827684
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 4.1%;
Best Local Similarity 48.0%;
Matches 110; Conservative
                                                                                                                                                     GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: 608-251-9166
INFORMATION FOR SEQ ID NO: 1:
                                                                                APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
LENGTH: 6243 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELECOMMUNICATION INFORMATION:
TELEPHONE: 608-251-5000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
                                                   APPLICANT:
                                                                                                                                                                                                                                                                     APPLICANT: Hopkins, TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
   TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                 884 gtaattaattagattcgtgtttttctcgattaataaactataagtttat 932
                                                                                                                                                                                                                                                                                                                                                        764 ttatttttcttctgtaataatctttgctttgatttttcttttaacaaaatccaaatgtag 823
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       704 ttgaatccatgaagaagacgatgatgatgatgatcattgttttcaccaaagtactta 763
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: misc_feature
LOCATION: 3770..4013
OTHER INFORMATION: /note= "RP4 origin of DNA transfer (oriT) from
OTHER INFORMATION: plasmid RP4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STREET: 1 Sout
CITY: Madison
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Seay, Nicholas J.
REGISTRATION NUMBER: 27
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                     53701-2113
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1 South Pinckney Street
                                                              Sreekrishna, Kotikanyadanam
Prevatt, William D
Thill, Gregory P
Davis, Geneva R
Koutz, Patricia
                                Hopkins,
                                                   Barr, Kathryn A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       linear
Production of Bacillus
Methylotrophic Yeast
                                  Sharon
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Pred. No. 1.1;
0; Mismatches 119;
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                    Entomotoxins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 6243;
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US-08-181-271A-36/c
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US-08-231-342-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Sin
Matches 64;
                                                                                                                                                                                                                                       Sequence 36, Application US/08181271A Patent No. 5614395
                                                                                                                                                                                                                     GENERAL INFORMATION:
                                                                                                                                                                                                                                     tent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NFORMATION FOR SEQ ID NO: 5:
                                                                                                                                                                                                                                                                                                                                                                                     1113 TTAGTTTTGATCATCTGTAATAATCTTTGTATTTCCTAGTAAAGGTTCACTTGCAAAATG 105
                                                                                                                                                                                                                                                                                                                             1053 TGGATATCTTGCTATTGTTGTATAGTTATCGTTTAAAGCAACCCCATG 1007
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                                                                                               APPLICANT:
                                                                                                                                           APPLICANT:
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COMPUTER READABLE FORM:
TYPE: Floppy disk
                                 APPLICANT:
                                                APPLICANT:
                                                                               APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-372-7842
TELEFAX: 312-372-7848
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
NAME: Feder, Scott B
REGISTRATION NUMBER: 33,:
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                        821 tagatatctttctctcgaataatcaataacatgtaattcaacttttg 867
                                                                                                                                                                                                                                                                                                                                                                                                                 761 trattatttttcttctgtaataatctttgctttgatttttcttttaacaaaatccaaatg 820
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CORRESPONDENCE ADDRESS:
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CITY: C
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC
OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
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Sperison, Christoph
Stinson, Jeffrey R.
                                                                             Meins, Jr., Frederick
Montoya, Alice
                                                                                                                       Friedrich, Leslie B. Goodman, Robert M.
                                                                                                                                                         Duesing,
                             Payne, George B.
                                              Neuhaus, Jean-Marc
                                                             Moyer, Mary B.
                                                                                                       Harms, Christian
                                                                                                                                                                        Beck, James
                                                                                                                                                                                  Ryals, John A.
Alexander, Danny C.
                                                                            Montoya,
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IBM PC compatible YSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                S. LaSalle St.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4.1%;
                                                                                                                                                         John H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Even, Tabin & Flannery
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 38.2;
Pred. No. 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0.81;
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TELEFAX: (919)541-8689
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                 TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                        FILING DATE: 7-SEP-1990 PRIOR APPLICATION DATA: APPLICATION NUMBER: US
                                                                                                                                                                                                                                                                                                                                          FILING DATE: 27-SEP-
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: 1-APR-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/678,378
                                                                                                                                     ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                     FILING DATE: 24-MAR-1989 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: 6-MAR-1992 PRIOR APPLICATION DATA:
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PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: US 08/093,301
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FILING DATE: 6-FEB-1
PRIOR APPLICATION DATA:
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FILING DATE: 6-NOV-1:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Williams, Shericca C.
TITLE OF INVENTION: CHEMICALLY REGULATABLE AND ANTI-PATHOGENIC TITLE OF INVENTION: DAS SEQUENCES AND USES THEREOF NUMBER OF SEQUENCES: 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
                                                                                                   NAME: Elmer, James : REGISTRATION NUMBER:
                                                                                                                                                                                                                                                          FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: FILING DATE: 20-OCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: FILING DATE: 21-DE
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                                                 TELEPHONE:
                                                                                       REFERENCE/DOCKET NUMBER:
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SOFTWARE: PatentIn
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                                 (919)541-8689
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                                                   (919)541-8614
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER: US 07/165,667
8-MAR-1988
                                                                                                                   James Scott
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Floppy disk
                                                                                                                                                                                                                                                          20-JUN-1989
                                                                                                                                                     12-APR-1993
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Release #1.0, Version #1.25
                                                                                                                                                                     US 08/045,95
                                                                                                                                                                                                                     US 07/329,018
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                   36:
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TYPE:

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US-08-449-315-36/c
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US-08-181-271A-36
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Best Local :
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                                                    COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Ver
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/449,315
FILING DATE: 24-MAY-1995
CLASSIFICATION BOTO
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/181,271
APPLICATION NUMBER: 08/181,271
FILING DATE: 13-JAN-94
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OKGANISM: CUCUMIS SATIVUS
INDIVIDUAL ISOLATE: Cucumber Chitinase Genomic
IMMEDIATE SOURCE:
CLONE: PEGALICIA
                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT:
APPLICANT:
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                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES: 106
CORRESPONDENCE ADDRESS:
ADDRESSEE: CIBA-GEIGY Corporation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: 1
                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION:
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PRIOR APPLICATION DATA:
APPLICATION NUMBER:
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CITY: H
STATE:
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Local Similarity 58.48;
hes 66; Conservative
                           APPLICATION NUMBER: FILING DATE: 16-JU
                                                                                                                                                                                                                                                               COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear
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5650505
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: New York
                                                                                                                                                                                                                                                   10532
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                                                                                                                                                                                                                                                                                                         7 Skyline Drive
                                                                                                                                                                                                                                                               USA
                                                                                                                                                                                                                                                                                                                                                                                                      Williams,
                                                                                                                                                                                                                                                                                                                                                                                                                                 Uknes,
                                                                                                                                                                                                                                                                                                                                                                                                                                               Sperison, Christoph
Stinson, Jeffrey R.
                                                                                                                                                                                                                                                                                                                                                                                                                       Ward,
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Moyer, Mary B.
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Harms, Christian
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                                                                                                                                                                   PatentIn Release #1.0, Version #1.25
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CHEMICALLY REGULATABLE AND ANTI-PATHOGENIC DNA SEQUENCES AND USES THEREOF
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US 07/937,197
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Best Local Similarity
Matches 66; Conserv
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/848,506
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FILING DATE: 12-APR-1993
ATTORNEY/AGENT INFORMATION:
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REGISTRATION NUMBER: 36,129
REFERENCE/DOCKET NUMBER: S-
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Search completed: January 30, 2002, 11:54:29 Job time: 2808 sec

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gb_Dat:AXX008799
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p_p1:AB029483
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-DB-GenEmb1 -OFMT-fastap -SUFFIX-p2n.rge -GAPOP-12.00.0
-GAPEXT=4.000 -MINMATCH-0.100 -LOCPCL-0.000 -LOCPEXT=0.000
-QGAPOP-4.500 -QGAPEXT=0.050 -XGAPOP-10.000 -XGAPEXT=0.500
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                                        I AP001510 Bacillus halodurans
AF269730 Staphylococcus epider
AX145048 Sequence 3770 from Pa
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gb_pr:HSU89942
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                 1 MetAlaAlaValArgArgArgGluArgAspValValGluGluAsnGlyVa 17
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Ratio: 5.091
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The Plant journal : for cell and molecular biology. 21 (4), 379-385
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Submitted (20-DEC-1999) Fobert
Plant Biotechnology Institute,
Saskatchewan S7N OW9, CANADA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

1 (bases 1 to 855)
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1114 C 228 g 249 t
                                                                                                                                                                                                                                                                                                                                                                                                                                      /evidence-experimental product="Cdc2a-interacting /protein_id="CAB76424.1" /db_xref="GI:7160669" /db_xref="SPTREMBL:Q9SCR2"
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SOURCE
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LOCUS A98054
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                                                                                                                                                                                                                                                Sequence 1 from Patent WO9914331.
A98054
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De, A. J. and De, V. L.
CYCLIN-DEPENDENT KINASE INHIBITORS AND USES THEREOF
PATENT: WO 9914331-A 1 25-MAR-1999;
ALMEIDA JANICE DE (BE); LANDRIEU ISABELLE (BE)
LOCATION/Qualifiers
                                                                                                                                                                                                 unidentified
                                                                                                                                                                                                                                    A98054.1 GI:6781292
                                                                                                                                                                                     unclassified
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/db_xref="taxon:32644"
                                             /note="unnamed protein product"
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On Jan 27, 2000 this sequence version replaced gi:6434247.
Information on performance of analysis and a more detailed annotation of this entry and other sequences of chromosomes 3, 4 and 5 can be viewed at: http://www.mips.biochem.mpg.de/proj/thal/.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EU Arabidopsis sequencing, project.
Direct Submission
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bloecker, H., Mewes, H.W., Lemcke, K., Mayer, K.F.X., Quetier, F. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Arabidopsis thaliana DNA chromosome 3, BAC
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IEFVDLEENNGDDRETETSWIYDDLNKSEESMNMDSSSVAVEDVESRRRLRKSLHETV
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                       intron
                                                                                                                                                                                                                                                                                                                                                                                                                         /translation="mfetehhtllpllllpsllsllflllkrnnktrfnlepgks gwefloetigylkpynattlgdemgqhyskygkiyrshlepept vsadaglurefilg negrlfecsyprsiggilgkwsklylvgdmhrdmrsislheflsharletillkdyerh tlfvldswqqhsifsaqdeakketynlmkakhinsmDpgeeteQlkkeyvjemkGyvs aplnlpgtayhkalqsratilkfierkmeerkldikeEDQeeeEvktedeaemsksdh
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/number=3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="Contains Cytochrome P450 cysteine heme-iron ligand
signature AA455-464; Prokaryotic membrane lipoprotein lipid
attachment site AA320-330"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          complement(join(26093. .26338,27091. .27200,27308. .27386,
27478. .27570,27723. .28037,28136. .28288,28374. .28698,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /translation="MAYMCTDSGNLMAIAQQLIKQKQQQQSQHQQQEEQEQEPNPWPN PSFCFTLPGSGFSDFFQVTNDPGFHFPHLEHHQNAAVASEEFDSDEWMESLINGGDAS QTNPDFF 17GHDPFV5FPSRLSAPSYLNRVNDDASAGQLEPPPPASTAIWSPSPPSPQ HPPPPPPQDFDLNQFIFKAIHDYAKKPETKPDTLIRIKESVSESGDPIQRVGYYFAE ALSHKETESPSSSSSSSSLEDFILSYKTLNDACPYSKFAHLTANQAILEATNQSNNIHI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /product="putative protein"
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MPSADPAFSYTDYSMIPADEIFLKGKILPFKETSHVHRTLGEELLTEEEGSMVDGNTF
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/note="similarity to predicted proteins, Arabidopsis
                                                                   complement(27308
                                                                                                                    complement(27201.
                                                                                                                                                                                                                   complement (26339.
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RSLNPRI VTLGEY EVSLNRVEFANRVKNSLRFY SAVFESLEPNLDRDSKERLRVERVL
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                                                                                                 /number-2
                                                                                                                                                                  complement (27091.
                                                                                                                                                                                                                                                                                                                             NYMPFGGGPRLCAGSELAKLEMAVFIHHLVLKFNWELAEDDKPFAFPFVDFPNGLPIF
                                                                                                                                                                                                                                                                                                                                                      \mathtt{RYKGYDIPSGWKVLPVISAVHLDNSRYDQPNLFNPWRWQQQNNGASSSGSGSFSTWGN}
                                                                                                                                                                                                                                                                                                                                                                        EELREEHLEIARAKKELGESELNWDDYKKMDFTQCVINETLRLGNVVRFLHRKALKDV
                                                                                                                                                                                                                                                                                                                                                                                                VRKQRTDDDLLGWYLKHSNLSTEQILDLILSLLFAGHETSSVAIALAIFFLQACPKAV
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                                                                                                                                                                                                   /number=
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alignment_scores:
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    Ratio:
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US-09-574-735C-2 x ATT3A5
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34 alGluSerArgIleIleLeuSerProCysValGlnAlaThrAsnArgGly 50
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73.077
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/number=4
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complement(38797. .38876)
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complement(28374.
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Percent Identity: 72.727
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208 AsnPro 209 13189 AATCCA 13194 seq_name: gb_pat:AX008796 seq_documentation_block: LOCUS	187	164 luLeuGluAspPhePheGlnValAlaGluLysAspLeuArgAsnLysLeu	39 GTCTCGCCGCAGGTTAAGGAAGACTCCATGAGACGGTGAAGGAAG	ASPLeuASDLySGATTTGTTAC.	108	84 luGluAspSerSerValSerCysCysSerThrSerGluGluLysSerLys	
06-SEP-2000	P 191 T 13138 U 207 		12 16 16	. 129 A 12838 II 130 II 12888	. 108 C 12738 C 12738 S 125 I 12788	s 100 A 12638 - 108 T 12688	T 12488 1 67 1 67 1 12538 1 12538 1 12538 1 1 12538

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alignment_scores:
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Percent Similarity: 100.000
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                                                                                                           ACGGAGAATCGAATTTGTAGATCTTGAGGAAAATAACGGTGACGATCGTG
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yArgTyrGluTrpValLysLeuAsnPro 209
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                                                                               TCTATGAAGTATAACTTCGATTTCGAGAAAGATGAGCCACTTGGTGGAGG
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1 (bases 1 to 755)

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/db_xref="taxon:3702"
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seq_name:

gb_p1:ATU94772

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VERSION
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                                                                                                                                                                                                                                                                                                                                                                                                             alignment_block:
US-09-574-735C-2 x ATU94772
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Quality:
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LOCUS ATU94772
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                                                                                                                                                                                 77 luGluGlnCysGlnIleGluGluAspSerSerValSerCysCysSer
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uAsnAsnGlyAspAspArgGluThrGluThrSerTrpIle.........
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GGAAGAT...AAAGATGGTGACACTGAAACGTCGACGTATCGACGGGTA
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                                                                                                           ThrSerGluGluLysSerLysArgArgIleGluPheValAspLeuGluGl
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                                                                                                                                                CC.....GTCGTCGGTGATAATGGAGTTTCGTCGTCTTGTAGTGGA
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheop
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

1 (bases 1 to 856)
Wang, H., Fowke, L.C. and Crosby, W.L.
A plant cyclin-dependent kinase inhibitor gene
Nature 386 (6624), 451-452 (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Arabidopsis thallana cyclin-dependent kinase inhibitor protein (ICKI) mRNA, complete cds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /translation="MVRKYRKAKGIVEAGVSSTYMQLRSRRIVYVRSEKSSSVSVVGD
NGVSSSCSGSNEYKKKELIHLEEEDKOGDTETSTYRRGTKRKLCENLREEEKELSKS
MENYSSEFESAVKESLDCCCSGRKTMEETVTAEEEEKAKLMTEMPTESEIEDFFVEAE
KQLEEKFKKKVNFDFEKEKPLEGRYEMVKLE"
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/strain="Columbia"
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alignment_block:
US-09-574-735C-2 x AX008791
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                                                                                                                                                                                                                                                                                                                                                                                      Fowke, L.C., Wang, H. and Crosby, W.L.

Cyclin-dependent kinase inhibitors as plant growth regulators

Patent: WO 9964599-A 1 16-DEC-1999;

FOWKE LARRY C (CA); WANG HONG (CA); AGRICULTURE AND AGRIFOOD CANAD

(CA); CANADA NAT RES COUNCIL (CA); CROSBY WILLIAM L (CA); UNIV

SASKATCHEWAN TECHNOLOGIES (CA)

LOCATION/Qualifiers
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cyclin dependent kinase inhibitor.
pisum sativum axillary bud cDNA to mRNA.
pisum sativum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AB029483 927 bp mRNA pLN 11-JAN-2001 pisum satiyum cki mRNA for cyclin dependent kinase inhibitor,
   inhibitor (CKI) homologue published Only in DataBase (2001) In press 2 (bases 1 to 927) Shimizu-Sato,S. and Mori,H.
                                                                                                                                                                                                                                                                             Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyt
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Vicieae;
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146 ValGluSerArg...ArgArgLeuArgLysSerLeuHisGluThrValLy 161
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                                                                                          luGluSerMetAsnMetAsp.....SerSerSerValAlaValGluAsp 145
                                                                                                                                                                                                                                     CTCGATGAAGAAAGGATCAAATCGTTAGATCTGGAGGTGGAGAGCGCGCA
                                                                                                                                                                                                                                                              LysSerLysArgArgIleGluPheValAspLeuGluGluAsnAsnGlyAs 114
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                                                                                                                                        AGGT...GAAACGTCGACGTGCAATTGCGATGAAGAAATTGAGAGGAGAG
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                              .....TyrAspAspLeuAsnLysSerGluG 132
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

1 (bases 1 to 660)
Fowke, L. C., Wang, H. and Crosby, W. L.
Cyclin-dependent kinase inhibitors as plant growth regulators
Patent: WO 9964599-A 3 16-DEC-1999;
FOWKE LARRY C (CA); WANG HONG (CA); AGRICULTURE AND AGRIFOOD CANAD
(CA); CANADA NAT RES COUNCIL (CA); CROSBY WILLIAM L (CA); UNIV
SASKATCHEMAN TECHNOLOGIES (CA)
SASKATCHEMAN TECHNOLOGIES (CA)
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                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (31-OCT-2000) De Veylder L., Departement Plantegenetica, Vlaams Interuniversitair Instituut voor Biologie (VIB), K.L. Ledeganckstraat 35, B-9000 Gent, BELGIUM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              De Veylder,L., Beeckman,T., Beemster,G.T., Krols,L., Terras,F., Landrieu,I., Van Der Schueren,E., Maes,S., Naudts,M. and Inze,D. Functional Analysis of Cyclin-Dependent Kinase Inhibitors of
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Arabidopsis thaliana
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The Plant cell. 13 (7),
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a 130 c 142 g 129 t
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alignment_scores:

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thale cress.
Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
                                                                                       Sequence 8 from AX008798
                                                                            AX008798.1 GI:9996262
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                                     188 snPheAspPheGluLysAspGluProLeuGlyGlyArgTyrGluTrp
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                                                                                                                       lAlaGluLysAspLeuArgAsnLysLeuLeuGluCysSerMetLysTyrA
                                                                                                                                                                                       SerLeuHisGluThrValLysGluAlaGluLeuGluAspPhePheGlnVa 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ACGAAATCGCTACTCGTCTTCCATTTTCAGATCTGGAGGCTCAT.....
ACTACGACATCGTCAATGATACGCCGCTT...GAAGGTCGGTACCAGTGG
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                                                                                                                                                                      AAGATGGAAAAATCACCGACGCAGGCAGAGCTTGATGACTTTTTCTCGGC
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1 (bases 1 to 642)

Fowke, L. C., Wang, H. and Crosby, W.L.

Cyclin-dependent kinase inhibitors as plant growth regulators

Patent: WO 9964599-A 8 16-DEC-1999;

FOWKE LARRY C (CA); WANG HONG (CA); AGRICULTURE AND AGRIFOOD CANAD

(CA); CANADA NAT RES COUNCIL (CA); CROSBY WILLIAM L (CA); UNIV

SASKATCHEWAN TECHNOLOGIES (CA)
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             leIleLeuSerProCysValGlnAlaThrAsnArgGlyGlyIleValAla
                                                             GAAGAAAACGAAGCTTAATGATTCTTCTGATTCATCACCGGACTCTCATG 109
                                                                                                   lLysArgArgLysMetGluGluGluValAsp...LeuValGluSerArgI 38
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Direct Submission

Submitted (31-OCT-2000) De Veylder L., Departement Plantegenetica,

Vlaams Interuniversitair Instituut voor Biologie (VIB), K.L.

Ledeganckstraat 35, B-9000 Gent, BELGIUM
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1 (bases 1 to 591)
1 (baylder, L., Beeckman, T., Beemster, G.T., Krols, L., Terras, F., Landrieu, I., Van Der Schueren, E., Maes, S., Naudts, M. and Inze, D. Functional Analysis of Cyclin-Dependent Kinase Inhibitors of
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/translation="MSERKRELAEEASSTSFSDLKKTKLNDSSDSSPDSHDVIVFAVS
/translation="MSERKRELAEEASSTSFSDLKKTKLNDSSDSSPDSHDVIVFAVS
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SELESQDDKKKQFIEKYNFDIVNDEPLEGRYKMDRL"
123 c 151 g 132 t
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/protein_id="CAC41620.1"
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/db_xref="taxon:3702"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          uThrGluThrSer...TrpIleTyrAspAspLeuAsnLys.....SerG 131
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            uLeuGluAspPhePheGlnValAlaGluLys.....AspLeuArgAsnL 179
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ArgIleGluPhe...ValAspLeuGluGluAsnAsnGlyAspAspArgGl 117
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Quality:
Ratio:
                                                                                                                                                                     1 (bases 1 to 824)

Fowke, L.C., Wang, H. and Crosby, W.L.

Cyclin-dependent kinase inhibitors as plant growth regulators

Patent: WO 9964599-A 7 16-DEC-1999;

FOWKE LARRY C (CA); WANG HONG (CA); AGRICULTURE AND AGRIFOOD CANAD

(CA); CANADA NAT RES COUNCIL (CA); CROSBY WILLIAM L (CA); UNIV

SASKATCHEWAN TECHNOLOGIES (CA)

LOCATION/Qualifiers
                                                                                                                                                                                                                                                                                                                                                            thale cress.
Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                             Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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                                                                                                    /organism="Arabidopsis thaliana"
/db_xref="taxon:3702"
164 c 185 g 188 t
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177.00
1.273
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Length:
Gaps:
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US-09-574-735C-2 x AX008797
                                                                                                                                                                        seq_name: gb_pat:AX008805
   REFERENCE
                                                                                    SOURCE
                                                                                                    KEYWORDS
                                                                                                                      VERSION
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                                                                                                                                      ACCESSION
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196 ProLeuGlyGlyArgTyrGluTrpValLysLeu 207
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        58 AGAAAGCGAGAGCTTGCAGAAGAAGCTTCAAGCACAAGCTTCTCACCACT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ysLeuLeuGluCysSerMetLysTyrAsnPheAspPheGluLysAspGlu 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CAGTGAGTGAGGGTTTGGGAGAAACGACAACAGAAATGGAATCATCATCG
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                                                                                                                                                                                                                                                                                                                                                                                            CCGCTT...GAAGGTCGCTACAAGTGGGATCGACTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SerArgArgAeuArgLysSerLeuHisGluThrValLysGluAlaGl 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   uThrGluThrSer...TrpIleTyrAspAspLeuAsnLys.....SerG 131
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Chenopodium rubrum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Caryophyllidae; Caryophyllales; Chenopodiaceae; Chenopodium.
1 (bases 1 to 804)
                                                                                                                                                                                                              Sequence 15 from Patent AX008805
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ACCESSION
VERSION
KEYWORDS
                                                                                            seq_documentation_block: LOCUS CRJ002173
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                                                                                                                                            seq_name: gb_pl:CRJ002173
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                                                                                                                                                                                    GATTGGGTTCCAATAAATCCA
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                                                                                                                                                                                                                                                           AGTACAATTTCGACATAGTTAAGGACGTGCCACTG...AAAGGTCGTTAT
                                                                                                                                                                                                                                                                                           ysTyrAsnPheAspPheGluLysAspGluProLeuGlyGlyGlyArgTyr 202
                                                                                                                                                                                                                                                                                                                                TGCTGTTGCTGAAAAAGATCTCCAGAAACGCTTCAGCGAA.....A 577
                                                                                                                                                                                                                                                                                                                                                       TCAACGGTACAGATCAAGATGCCGTCTGATTCAGAAATCGAAGAATTCTT
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Cyclin dependent kinase inhibitors as plant growth regulators
Patent: WO 9964599-A 15 16-DEC-1999;
FOWKE LARRY C (CA); WANG HONG (CA); AGRICULTURE AND AGRIFOOD CANAD
(CA); CANADA NAT RES COUNCIL (CA); CROSBY WILLIAM L (CA); UNIV
SASKATCHEWAN TECHNOLOGIES (CA)
complete cds.
AJ002173
AJ002173.1 GI:2653280
cyclin-dependent kinase inhibitor.
                                                                      Chenopodium rubrum
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                                                                                        CRJ002173
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1.768
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/db_xref="taxon:3560"
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GCCG.....
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Submitted (25-NOV-1997) Fountain M.D., Plant Physiology, of Bayreuth, Universitaetstrasse 30, 95447, GERWANY
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1 (bases 1 to 804)
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/product-_cyclin-dependent kinase inhibitor protein"
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tissue"
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/dev_stage="7 day
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/db_xref="taxon:3560"
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US-09-574-735C-2 x AX008795
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                                                  131 TGTTGTAGCGGGAGGAAAACGATGGAGGAGGAGGAGGAGGAGGAGGCGAAATT 180
155 rLeuHisGluThrValLysGluAlaGluLeuGluAspPhePheGlnValA 172
                                                                                                                                                                                            132 luSerMetAsnMetAspSerSerSerValAlaValGluAsp...... 145
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ISM Arabidops is thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Eukaryota; Viridiplantae; eudicotyledons; core eudicots;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

[CE 1 (bases 1 to 377)

RS FOWKe, L.C., Wang, H. and Crosby, W.L.
Cyclin-dependent kinase inhibitors as plant growth regulators
Cyclin-dependent kinase inhibitors as plant growth regulators
Cyclin-dependent kinase inhibitors as plant growth regulators
FOWKE LARRY C (CA); WANG HONG (CA); AGRICULTURE AND AGRIFOOD CANAD
FOWKE LARRY C (CA); WANG HONG (CA); AGRICULTURE AND AGRIFOOD CANAD
(CA); CANADA NAT RES COUNCIL (CA); CROSBY WILLIAM L (CA); UNIV
CA); CANADA NAT RES COUNCIL (CA); CROSBY WILLIAM L (CA); UNIV
SASKATCHEWAN TECHNOLOGIES (CA)
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                                                                                                                                                  Quality:
Ratio:
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/db_xref="taxon:3702"
31 c 109 g 99 t
                                                                                             .....ValGluSerArgArgArgLeuArgLysSe 155
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Ratio: 5.091
Percent Similarity: 100.000
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                                                                                                                                                                                                          luGluAspSerSerValSerCysCysSerThrSerGluGluLysSerLys
                                                                                                                          ArgArgIleGluPheValAspLeuGluGluAsnAsnGlyAspAspArgGl 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          99US-0155659
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Gaps: 0
Percent Identity: 100.000
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08-JUL-1999
10-JUL-1999
11-JUL-1999
12-JUL-1999
13-JUL-1999
13-JUL

99US-0142803
99US-0142977
99US-0144297
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99US-0154039

457

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seq_name: /SIDS2/gcgdata/geneseq/geneseqn/NA1999.DAT:AAX25015
                                                                                                                                                                                                                                                                                                                                                                                                                                                    _documentation_block:
                                                                                                                                                                                                                                                                                                                                    Cyclin-dependent kinase inhibitor; CDK inhibitor; CKI; CDKI; FL39; plant development; transgenic plant; cell cycle; growth regulator; herbicide; ds.
                                                                                                                                                                                                                                                                                             Key
Claim 1b; Page 72-74; 88pp; English.
                                                                                                               24-DEC-1997;
16-SEP-1997;
                                                                                                                                                                                                                                          misc_teature
                                                                                                                                                                                                                                                                                                                                                                                                                       AAX25015;
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                    DNA encoding inhibitor of cyclin-dependent kinase
                                                    WPI; 1999-229535/19.
                                                                      De Almeida J,
                                                                                                                                              16-SEP-1998;
                                                                                                                                                                   25-MAR-1999.
                                                                                                                                                                                       W09914331-A2
                                                                                                                                                                                                                                                             polyA_signal
                                                                                                                                                                                                                                                                                                                                                                              Arabidopsis cyclin-dependent kinase inhibitor FL39 cDNA clone
                                                                                                                                                                                                                                                                                                                                                                                                                                            AAX25015 standard; cDNA; 932
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            184
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          458
                                                                                           (CROP-) CROPDESIGN NV.
                                                                                                                                                                                                                                                                                                                Arabidopsis thaliana.
                                                                                                                                                                                                                                                                                                                                                                                                  05-JUL-1999 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      etAsnMetAspSerSerSerValAlaValGluAspValGluSerArgArg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ArgLeuArgLysSerLeuH1sGluThrValLysGluAlaGluLeuGluAs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   uThrGluThrSerTrpIleTyrAspAspLeuAsnLysSerGluGluSerM 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ArgTyrGluTrpValLysLeuAsnPro 209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TGAACATGGATTCTTCGGTGGCTGTTGAAGATGTAGAGTCTCGCCGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AGGTTAAGGAAGACTCTCCATGAGACGGTGAAGGAAGCTGAGTTAGAAGA
                                          AAW98179
                                                                      De Veylder
                                                                                                              97EP-0204111.
97EP-0202838.
                                                                                                                                              98WO-EP05895
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915..920
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305..932
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/note= "this region of the sequence
claimed in Claim 1(c)"
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CC cyclin-dependent kinase (CDK) inhibitor (see AAW98179) of Arabidopsis CC thaliana. New plant products with a putative CDK inhibitory CC function were screened by using a two-hybrid system with CDC2aAt CC function were screened by using a two-hybrid system with CDC2aAt CC protein as bait and a library made from an RNA mixture of A. CC thaliana cell suspensions harvested at the early exponential, carly stationary and stationary phases. Positive CC exponential, early stationary and stationary phases. Positive CC clones LDV39, LDV66 and LDV159 were obtained. Clone FL39 was CC isolated from a flower CDNA library using partial clone LDV39 as CC isolated from a flower CDNA library using partial clone LDV39 as CC isolated from ALFCDKI (see AAX25018), was obtained from CC alfalfa. Results established that several CDK inhibitors exist concent the points and may have different functions during the development CC isolated recombinant DNA and vectors are all useful: for CC diagnosis (no details); for modulating the cycle, division and/or CC growth of plant cells; for altering activity of CDK; for modulating cromoter inhibition in plants caused by environmental stress; for CC inducing male or female sterility; for altering cell division cells; cand to screen for agonists or antagonists that are potentially CC useful as growth regulators or herbicides. Plants of any sort can be treated, e.g. to alter their size or resistance to disease.

XX Sequence 932 BP; 289 A; 125 C; 254 G; 264 T; 0 other;
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Quality: 1064.00 Length: 209
Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000
alignment_block:
US-09-574-735C-2 x AAX25015
Align seg 1/1 to: AAX25015 from: 1 to: 932

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101
                                                                                                                                                                                                                                                                                         286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             136 TACGACGACGGTGAAACGAAGGAAGATGGAGGAAGTGGATTTAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                  186 TGGAATCTAGGATAATTCTGTCTCCGTGTGTACAGGCGACGAATCGCGGT
                                                                                                                                                                                                                               84 luGluAspSerSerValSerCysCysSerThrSerGluGluLysSerLys
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         86 ATGGCGGCGGTTAGGAGAAGAGAACGAGATGTGGTTGAAGAGAATGGAGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 MetAlaAlaValArgArgArgGluArgAspValValGluGluAsnGlyVa
etAsnMetAspSerSerSerValAlaValGluAspValGluSerArgArg
                                                        eValArgArgArgAspSerProProValGluGluGlnCysGlnIleGluG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    alGluSerArgIleIleLeuSerProCysValGlnAlaThrAsnArgGly
                                                                                                                                                    ArgArgIleGluPheValAspLeuGluGluAsnAsnGlyAspAspArgGl 117
                                                                                                                                    CGGAGAATCGAATTTGTAGATCTTGAGGAAAATAACGGTGACGATCGTGA
                                                                                                                                                                                                               AAGAAGATTCGTCGGTTTCGTGTTCTACATCGGAAGAGAAATCGAAA
                                                                                                                                                                                                                                                                                                                                                                      GGAATTGTGGCGAGAAATTCAGCAGGAGCGTCGGAGACGAGTGTTAT
                                                                                                                                                                                                                                                                                         AGTACGACGCCGAGATTCTCCTCCGGTTGAAGAACAGTGTCAAATCGAAG
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gene in a plant. BRO4 is useful for increasing the proportion of dividing cells in a plant cell population comprising protoplast, seeds, root cells, meristem cells or leaf cells.

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seq_name: /SIDS2/gcgdata/geneseq/geneseqn/NA2001.DAT:AAC85204
     The sequence given in AAC85204 represents a plant D1 cyclin inhibitor gene, BRO3. This sequence was isolated using a yeast two hybrid screen. The BRO3 protein was found to contain a seven amino acid sequence cyclin binding domain similar to that of BRO1, BRO2 and BRO4 (See also AAB47005-6). This sequence is homologous to a sequence present in a D-like cyclin inhibitor gene and when integrated at the corresponding locus, functionally inactivates plant D-like cyclin inhibitor protein expression. The BRO4 coding sequence may be used to produce a hyperplastic variant plant, increase the growth rate of a plant, or increase the proportion of dividing cells in a plant cell population, relative to a wild-type plant, by functionally increase the proportion of dividing cells in a plant cell population, relative to a wild-type plant, by functionally
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       _documentation_block:
                                                                                                                                                                                                                                                 Functionally inactivating expression of plant D-like cyclin inhibitor gene for producing a hyperplastic variant plant, modulating the growth and/or yield of plants, and increasing the proportion of dividing cells
                                                                                                                                                                                                                     Example 1; Page 39-40; 50pp; English.
                                                                                                                                                                                                                                                                                                                                           WPI; 2001-024998/03.
                                                                                                                                                                                                                                                                                                                                                                                                          (HUTC-) HUTCHINSON CANCER RES CENT FRED
                                                                                                                                                                                                                                                                                                                                                                                                                                            14-MAY-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             15-MAY-2000; 2000WO-US13379
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Plant; D-like cyclin inhibitor gene; BRO4; hyperplastic; variant; growth rate; dividing cells; inactivation; protoplast; seed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          586
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Arabidopsis thaliana.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   root cell; meristem; leaf; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Plant D-like cyclin inhibitor BRO3 coding sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAC85204;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAC85204 standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       erMetLysTyrAsnPheAspPheGluLysAspGluProLeuGlyGlyGly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TTTTTTCAGGTGGCGGAGAAAGATCTTCGGAATAAGTTGTTGGAATGTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CTATGAAGTATAACTTCGATTTCGAGAAAGATGAGCCACTTGGTGGAGGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers 69..620
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the expression

of a

plant D-like cyclin inhibitor

seq_documentation_block:
ID AAZ29416 standard;

AAZ29416 standard; cDNA; 755 BP

seq_name: /SIDS2/gcgdata/geneseq/geneseqn/NA2000.DAT:AAZ29416

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alignment_block:
US-09-574-735C-2 x AAC85204
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615
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              luLysAspGluProLeuGlyGlyGlyArgTyrGluTrpValLysLeuAsn
                                                                             GluGluAsnAsnGlyAspAspArgGluThrGluThrSerTrpIleTyrAs
                                                                                                                                                                                                                                                                                                                    CCA
                   Pro 209
                                                                                                                    ThrValLysGluAlaGluLeuGluAspPhePheGlnValAlaGluLysAs
                                                                                                                                                                    laValGluAspValGluSerArgArgArgLeuArgLysSerLeuHisGlu
                                                                                                                                                                                                            PASpLeuAsnLysSerGluGluSerMetAsnMetAspSerSerSerValA
                                                                                                                                                                                                                                        GAGGAAAATAACGGTGACGATCGTGAAACAGAAACGTCGTGGATTTACGA
                                                                                                                                                                                                                                                                                                                                                                                                   CGTGTGTACAGGCGACGAATCGCGGTGGAATTGTGGCGAGAAATTCAGCA
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                                      AGAAAGATGAGCCACTTGGTGGAGGAAGATACGAGTGGGTTAAATTGAAT
                                                                                                                                                           CTGTTGAAGATGTAGAGTCTCGCCGCAGGTTAAGGAAGAGTCTCCATGAG
                                                                                                                                                                                                TGATTTGAATAAGAGTGAGGAATCGATGAACATGGATTCTTCTTCGGTGG
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617
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5.109
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Gaps:
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alignment_block:
US-09-574-735C-2
                                                                                                                                                             alignment_scores:
                                                                                                                            Ratio:
Percent Similarity:
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                                                                                                                                                                                                              The present sequence is a cDNA encoding ICK2 which inhibits A. thaliana Cyclin-Dependent kinase (CDK). Interactor of Cdc2 kinase 2 (ICK2) interacts with Cdc2a, b-class cyclins, CycD1, CycD2 and CycD3 and shares functional and sequence similarity with ICK1. Growth, morphogenesis, multiplication, enlargement, differentiation and maturation of plant cells can be modified by transforming them with nucleic acid encoding CDK inhibitor or antisense construct complementary to the inhibitor gene, operably linked to a tissue-specific promoter. The transgenic plants exhibit alteration of traits such as petals, male sterility and ability to set seeds.
                                                                                                                                                                                                                                                                                                                                                        Modifying plant cell development using nucleic acid encoding inhibitor of cyclin-dependent kinase, or corresponding antisense sequence, e.g. for inducing male sterility -
                                                                                                                                                                                                                                                                                                                                                                                                                                  Wang
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Cyclin-Dependent kins
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                51 GlyIleValAlaArgAsnSerAlaGlyAlaSerGluThr.......
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31-DEC-1998;
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                       AGCAATGAATATAAGAAGAAA.
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DB; AAY44335.
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98CA-2256121.
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The present sequence is a cDNA encoding A. thaliana Cyclin-Dependent kinase (CDK) inhibitor, ICK1. Interactor of Cdc2 kinase 1 (ICK1) interacts with Cdc2a, D-class cyclins, CycD1, CycD2 and CycD3. Growth, morphogenesis, multiplication, enlargement, differentiation and maturation of plant cells can be modified by transforming them with nucleic acid encoding CDK inhibitor or antisense construct complementary to the inhibitor gene, operably linked to a tissue-specific promoter. The transgenic plants exhibit alteration of traits such as petals, male sterility and ability to set seeds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Modifying plant cell development using nucleic acid encoding inhibitor of cyclin-dependent kinase, or corresponding antisense sequence, e.g. for inducing male sterility
                                                                                                                                                                                        123 ACGGAGCCGGAGAATTGTTTATGTTAGATCGGAAAAATCAAGCTCTGTCT
                                          94 ThrSerGluGluLysSerLysArgArgIleGluPheValAspLeuGluGl 110
                                                                                                                                                                                                                                                                                                                luGluGlnCysGlnIleGluGluGluAspSerSerValSerCysCysSer
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.GAATTAATACATCTGGAGGA
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254
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seq_name: /SIDS2/gcgdata/geneseq/geneseqn/NA2000.DAT:AAZ29418
                                                                                                                                                                                                                                                                                          Cyclin-Dependent kinase inhibitor; CDK; Interactor of Cyclin 6; ICN6; Cdc2a; D-class cyclin; CycD1; CycD2; CycD3; morphogenesis; antisense construct; tissue-specific promoter; transgenic plant; male sterility; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Arabidopsis thaliana CDK inhibitor, ICN6 encoding cDNA.
                                                                                                                                                                                                                                                                                                                                                                                                               AAZ29418 standard; cDNA; 642
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                                                                             AGRIC & AGRIFOOD CANADA.
UNIV SASKATCHEWAN TECHNOLOGIES
                                                                    NAT RES COUNCIL CANADA.
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                                                                                                              98CA-2235978.
98CA-2256121.
                                                                                                                                                99WO-CA00532
                                                                                                                                                                                                                /product= "ICN6"
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                                             Crosby WL
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alignment_block:
US-09-574-735C-2 x AAZ29418
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        130 ... CCGACGAGAACTCTTCTTCTTCTTCCTCTTCTTCTCTGGCTTACTCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 642 BP;
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lAlaGluLysAspLeuArgAsnLysLeuLeuGluCysSerMetLysTyrA 188
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                                                       SerLeuHisGluThrValLysGluAlaGluLeuGluAspPhePheGlnVa
                                                                                                                                                 erSerValAlaValGluAspValGluSerArgArgArgLeuArgLys
                                                                                                                                                                                                                                                                  GAAATCTCCGAAACCGAAATCTCAACGTTACTCACCAACAATTTCAGGAA
                                                                                                                                                                                                                                                                                                                                            ACGAAATCGCTACTCGTCTTCCATTTTCAGATCTGGAGGCTCAT.....
                                                                                                                                                                                                                                                                                                                                                                   LuLysSerLysArgArgIleGluPheValAspLeuGluGluAsnAsnGly
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                                                                                                                                                                                                                                                                                                                                                                                                                       CGATCATCTAAGCTCAAGCATCAGCTCTGGTTGTTCCAGCAGCGAAACTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GTTTCAGATTCCGGAGGTTTCTGCTCCGTCGCGTTATCTGAAGAAGAAGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              alAlaArgAsnSerAlaGlyAlaSerGluThrSerValValIleValArg
                                   AAGATGGAAAAATCACCGACGCAGGCAGAGCTTGATGACTTTTCTCGGC
                                                                                                               CGGCGACGACGAGATGAGAGAT...CAGAGAAAGACGGAGAAGAAGAAG
                                                                                                                                                                                          ACAGGGAATTTCATCAAGCGAGAATCTGGGAGAAACAGCAGAAATGGACT
                                                                                                                                                                                                                            .....LeuAsnLysSerGlu.......GluSerMetAsnMetAspS 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                       p......CysCysSerThrSerGluG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      rArgIleIleLeuSerProCysValGlnAlaThrAsnArgGlyGlyIleV 53
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Ratio:
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1.508
59.024
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9
27.805
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                                   518
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GGCGGAGAGATACGAACAGAAACGATTCACAGAA.....

AAGTACA

Percent Identity: 30.660

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alignment_scores:
Quality:
Ratio:
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ID AAC85201 standard; DNA; 626 BP.
XX
AC AAC85201;
XX
XX
XX
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                                                                                                                                                              The sequence given in AAC85201 represents a plant D-like cyclin inhibitor gene, BR04. This sequence may be used to produce a hyperplastic variant plant, increase the growth rate of a plant, or increase the proportion of dividing cells in a plant cell population, relative to a wild-type plant, by functionally inactivating the expression of a plant D-like cyclin inhibitor gene in a plant. This sequence is homologous to a sequence present in a D-like cyclin inhibitor gene and when integrated at the corresponding locus, functionally inactivates plant D-like cyclin inhibitor protein expression. BR04 is useful for producing hyperplastic variant plants, increasing the growth rate of a plant and for increasing the proportion of dividing cells in a plant cell population comprising protoplast, seeds, root cells, meristem cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Functionally inactivating expression of plant D-like cyclin inhibitor gene for producing a hyperplastic variant plant, modulating the growth and/or yield of plants, and increasing the proportion of dividing cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Plant; D-like cyclin inhibitor gene; BRO4; growth rate; dividing cells; inactivation; root cell; meristem; leaf; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            607
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 16; Page 41; 50pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               P-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2001-024998/03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Roberts J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          14-MAY-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              23-NOV-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Plant D-like cyclin inhibitor BRO4 coding sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         22-MAR-2001
                                                                                                          Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GTTAGTCTGAAACCT 621
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAB47001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HUTCHINSON CANCER
                                                                                                          626 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Kelly B;
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        177.00
1.273
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    Length:
Gaps:
                                                                                                          137 T; 0 other;
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    212
13
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Cyclin-Dependent kinase inhibitor; CDK; Interactor of Cyclin 2; ICN2; Cdc2a; D-class cyclin; CycD1; CycD2; CycD3; morphogenesis; antisense construct; tissue-specific promoter; transgenic plant;
                                                                                                                                                                                                                                                                                                                   591
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seq_documentation_block:
ID AAZ29417 standard; cD
XX AAZ29417;
AC AAZ29417;
XX 29-FEB-2000 (first e
XX Arabidopsis thaliana
XX Cyclin-Dependent kina
XX ICN2; Cdc2a; D-class
KW ICN2; Cdc2a; D-class
KW antisense construct;
                                                                                                                                                                                                                                                                                                                                                seq_name: /SIDS2/gcgdata/geneseq/geneseqn/NA2000.DAT:AA229417
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   alignment_block:
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                                                                                                        Arabidopsis thaliana CDK inhibitor, ICN2 encoding cDNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             550 AATTCATAGAA.....AAGTACAACTTCGATATTGTCAATGACGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         22 lLysArgArgLysMetGluGluGluValAsp...LeuValGluSerArgI 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                45 AGAAAGCGAGAGCTTGCAGAAGAAGCTTCAAGCACAAGCTTCTCACCACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               7 ArgGluArgAspValValGluGluAsnGlyValThrThr...ThrThrVa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               uLeuGluAspPhePheGlnValAlaGluLys.....AspLeuArgAsnL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ArgIleGluPhe...ValAspLeuGluGluAsnAsnGlyAspAspArgGl 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      erValSerCys...CysSerThrSerGluGluLys.....SerLysArg 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                      ProLeuGlyGlyArgTyrGluTrpValLysLeu 207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AGTTCGTCGTTTGGTGTAGATCTGGAGGATCATCAA...ATCGAAACCGA 349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    gAspSerProProValGluGluGlnCysGlnIleGluGluGluAspSerS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      leIleLeuSerProCysValGlnAlaThrAsnArgGlyGlyIleValAla
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                                                                                                                                                                                                                                                                                                                                                                                                       CCGCTT...GAAGGTCGCTACAAGTGGGATCGACTT 623
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ysLeuLeuGluCysSerMetLysTyrAsnPheAspPheGluLysAspGlu 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GATTGAGGATTTGTTCTCGGAGCTAGAGAGTCCAGACGATAAGAAGAAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GCAACGAAGAGAAAACAACCGGGGGGGGGAAGACTCCAACGGCGGCGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SerArgArgArgLeuArgLysSerLeuHisGluThrValLysGluAlaGl 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CAGTGAGTGAGGGTTTGGGGAGAAACGACAACAGAAATGGAATCATCATCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      luGluSerMetAsnMetAspSerSerSerValAlaValGluAspValGlu 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AACCGAAACCTCAACATTCATCACCAGCAATTTCAGAAAAGAGACGAGTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            uThrGluThrSer...TrpIleTyrAspAspLeuAsnLys.....SerG 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GTATCAGCTCCGGTTGTTTCACCAGTGAATCGAAAGAAATCGCGAAGAAC
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                                                                                                                                                                                                                                                                   CDNA; 824
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alignment_block:
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                                                                                                                                                                                                                                                                                          US-09-574-735C-2 x AAZ29417
                                                                                                                                                                                                                                                                                                                                     Percent Similarity:
196 TCGTCGGCGCTTTAGCGTCTGATGAATGTTCCGTTACCATCGGTGGAGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present sequence is a cDNA encoding ICN2 which inhibits A. thaliana Cyclin-Dependent Kinase (CDK). Interactor of Cyclin 2 (ICN2) interacts with GGC2a, D-class cyclins, CycD1, CycD2 and CycD3 and shares functional and sequence similarity with ICK1. Growth, morphogenesis, multiplication, enlargement, differentiation and maturation of plant cells can be modified by transforming them with nucleic acid encoding CDK inhibitor or antisense construct complementary to the inhibitor gene, operably linked to a tissue-specific promoter. The transgenic plants exhibit alteration of traits such as petals, male sterility and ability to set seeds.
                                                                  158
                                                                                                                                 108
                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 824 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Modifying plant cell development using nucleic acid encoding inhibitor of cyclin-dependent kinase, or corresponding antisense sequence, e.g. for inducing male sterility -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2000-097540/08.
P-PSDB; AAY44337.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; Fig 4; 58pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (MIAC ) AGRIC & AGRIFOOD CANADA.
(UYSA-) UNIV SASKATCHEWAN TECHNOLOGIES INC.
(CANA ) NAT RES COUNCIL CANADA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  08-JUN-1998;
31-DEC-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               08-JUN-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       male sterility;
                                                                                                                                                        22 lLysArgArgLysMetGluGluGluValAsp...LeuValGluSerArgI 38
                                                                                                                                                                                                58
                                                                                         leIleLeuSerProCysValGlnAlaThrAsnArgGlyGlyIleValAla 54
                                                                                                                            GAAGAAAACGAAGCTTAATGATTCTTCTGATTCATCACCGGACTCTCATG
                                                                                                                                                                                                              ArgGluArgAspValValGluGluAsnGlyValThrThr...ThrThrVa
                                                               ACGTCATCGTCTTCGCGGTTTCATCTTCC.......GTTGCT
                               ArgAsnSerAlaGlyAlaSerGluThrSerValValIleValArgArgAr 71
                                                                                                                                                                                           AGAAAGCGAGAGCTTGCAGAAGAAGCTTCAAGCACAAGCTTCTCACCACT 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     н,
                                                                                                                                                                                                                                                                                                                                                                      Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Fowke LC,
                                                                                                                                                                                                                                                                                                                                                       Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 98CA-2235978.
98CA-2256121.
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                                                                                                                                                                                                                                                                                                                                       177.00
1.273
65.566
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                                                                                                                                                                                                                                                                                                                                                                                                                                 287 A; 164 C; 185 G; 188 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /*tag= a
/product= "ICN2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers 1..639
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Crosby WL;
                                                                                                                                                                                                                                                          from: 1
                                                                                                                                                                                                                                                                                                                                     Gaps:
Percent Identity:
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                                                                                                                                                                                                                                                            824
                                                                                                                                                                                                                                                                                                                                     212
13
30.660
 245
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seq_documentation_block:
ID AAZ29420 standard; cDNA; 804 BP
XX
AAZ29420;
XX
DT 29-FEB-2000 (first entry)
XX
Chenopodium rubrum CDKII encodi
XX
Cyclin-Dependent kinase; CDK; C
KW CycD2; CycD3; morphogenesis; tr
XX
Chenopodium rubrum.
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FH Key Location/Qualif
FT CDS 58.648
FT CDS /*tag- a
FT CDS /*tag-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         seq_name:
                                                                                                                                       (MIAC ) AGRIC & AGRIFOOD CANADA.
(UYSA-) UNIV SASKATCHEWAN TECHNOLOGIES
(CANA ) NAT RES COUNCIL CANADA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cyclin-Dependent kinase; CDK; CDKI1; Cdc2a; D-class cyclin; CycC2; CycD3; morphogenesis; transgenic plant; male sterility;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Chenopodium rubrum CDKI1 encoding cDNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            563
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             513
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              463
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               413
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           117
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   131 luGluSerMetAsnMetAspSerSerSerValAlaValGluAspValGlu 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  71 gAspSerProProValGluGluGlnCysGlnIleGluGluGluAspSerS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ProLeuGlyGlyArgTyrGluTrpValLysLeu 207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                uLeuGluAspPhePheGlnValAlaGluLys.....AspLeuArgAsnL
|::::|||||:::|||:::
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ArgIleGluPhe...ValAspLeuGluGluAsnAsnGlyAspAspArgGl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CCGCTT...GAAGGTCGCTACAAGTGGGATCGACTT 636
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AATTCATAGAA.....AAGTACAACTTCGATATTGTCAATGACGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ysLeuLeuGluCysSerMetLysTyrAsnPheAspPheGluLysAspGlu 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GATTGAGGATTTGTTCTCGGAGCTAGAGAGTCAAGACGATAAGAAGAAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GCAACGAAGAGAAAACAACCGGGGGGTGAGGAAGACTCCAACGGCGGCGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SerArgArgLeuArgLysSerLeuHisGluThrValLysGluAlaGl 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CAGTGAGTGAGGGTTTGGGAGAAACGACAACAGAAATGGAATCATCATCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AACCGAAACCTCAACATTCATCACCAGCAATTTCAGAAAAGAGACGAGTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 uThrGluThrSer...TrpIleTyrAspAspLeuAsnLys.....SerG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AGTTCGTCGTTTGGTGTAGATCTGGAGGATCATCAA...ATCGAAACCGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      erValSerCys...CysSerThrSerGluGluLys.....SerLysArg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AGAAAGT......GATCAGTCCTCGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /rtag= a
/product= "CDKI1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers 58..648
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       512
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        462
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        131
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alignment_block:
US-09-574-735C-2 x AAZ29420
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  seq_name:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ratio:
Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present sequence is a cDNA encoding C. rubrum CDKI1, which inhibits Arabidopsis thaliana Cyclin. Dependent kinase (CDK). CDKII interacts with Cdc2a, D-class cyclins. CycD1, CycD2 and CycD3 and shares functional and sequence similarity with ICKI. Growth, morphogenesis, multiplication, enlargement, differentiation and maturation of plant cells can be modified by transforming them with Agrobacterium strain harbouring an expression construct of CDKII. The transgenic plants exhibit alteration of traits such as petals, male sterility and ability to set seeds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Modifying plant cell development using nucleic acid encoding inhibitor of cyclin-dependent kinase, or corresponding antisense sequence, e.g. for inducing male sterility -
                                                                                                                                                                                                                                                                                                                                  487
                                                                                                                                                                                                                                                                                                                                                                                                                          437
                                                                                                                                                                                        186
                                                                                                                                                                                                                                                                                   169
                                                                                                                                                                                                                                                                                                                                                                              154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          396
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  P-PSDB; AAY44340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      238 GCGAATTGCTCGAGTAGCGAGGTAATTACTACAGCTAGGTCGGATTTTCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure; Fig 6; 58pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     74 oProValGluGluGlnCysGlnIleGluGluGluAspSerSerValSerC 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  58 AlaGlyAlaSerGluThrSerValValIleValArgArgArgAspSerPr
                                                                       GluTrpValLysLeuAsnPro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ysCysSerThrSer...GluGluLysSerLysArgArgIleGluPheVal 106
                                            GATTGGGTTCCAATAAATCCA 645
                                                                                                                                       AGTACAATTTCGACATAGTTAAGGACGTGCCACTG...AAAGGTCGTTAT
                                                                                                                                                                  ysTyrAsnPheAspPheGluLysAspGluProLeuGlyGlyGlyArgTyr
                                                                                                                                                                                                                                    TGCTGTTGCTGAAAAAGATCTCCAGAAACGCTTCAGCGAA.....A
                                                                                                                                                                                                                                                                                eGlnValAlaGluLysAspLeuArgAsnLysLeuLeuGluCysSerMetL 186
                                                                                                                                                                                                                                                                                                                             TCAACGGTACAGATCAAGATGCCGTCTGATTCAGAAATCGAAGAATTCTT
                                                                                                                                                                                                                                                                                                                                                                         LysSerLeuHis...GluThrValLysGluAlaGluLeuGluAspPhePh 169
                                                                                                                                                                                                                                                                                                                                                                                                                        AAGCGAGAAGCTACAAAATTAGACGACCAGGATTATCCGGCGACGAAA 486
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      spSerSerSerValAlaValGluAspValGluSerArgArgArgLeuArg 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TGGT.....GAGGCGTCGTCAAAGCAAAAGGAGAGCCATAGAACAG 436
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 rSerTrpIleTyrAspAspLeuAsnLysSerGluGluSerMetAsnMetA 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAGGATGATGGTTTGGGAAATCGTACAGCAGATCCAGAGGTTGAGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AspLeuGluGluAsnAsnGlyAsp......AspArgGluThrGluTh 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GTTGCTCAAGCAATTATGATCAGTTGAGTTCTAGCGAGCCAGAAGTAGTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GCCG......TCTT
/SIDS2/gcgdata/geneseq/geneseqn/NA2000.DAT:AAC36219
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                804 BP; 254 A; 151 C;
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1.768
63.057
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ţo:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   804
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   157
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                                                                                                                                                                                     202
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Hybridisation assay; genetic mapping; gene expression control; protein identification; signal transduction pathway;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Arabidopsis thaliana DNA fragment SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                     pathway; promoter;
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AAA95288;
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DT 17-JAN-2001 (first e
XX Soybean cyclin-depend
XX Soybean; cyclin-depend
XX CDKI; cell growth; he
XX CO-APR-2000; 2000WO-U
XX DF 12-OCT-2000; 2000WO-U
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DR WPI; 2000
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The present sequence is the coding sequence for the soybean cyclin-dependent kinase inhibitor (CDKI). It was isolated by searching soybean pod cDNA library for sequences similar to those encoding the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Soybean; cyclin-dependent kinase inhibitor; cell cycle; cell division; CDKI; cell growth; herbicide; ss.
                                                                                                                                                                                                                              Cyclin dependent kinase inhibitor sequences, useful for identifying herbicides and plant growth inhibitors -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      06-APR-2000; 2000WO-US09106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Soybean cyclin-dependent kinase inhibitor coding sequence
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                                                                                                                                                        Claim 2; Page 49-50; 58pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAA95288 standard; cDNA; 1116 BP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                euLeuGluCysSerMetLysTyrAsnPheAspPheGluLysAspGluPro 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GluSerArgArgArgLeuArgLysSerLeuHisGluThrValLysGluAl 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CTTGGTGGAGGAAGATACGAGTGGGTTAAATTGAATCCA 437
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ..TTGGAATGTTCTATGAAGTATAACTTCGATTTCGAGAAAGATGAGCCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   aGluLeuGluAspPhePheGlnValAlaGluLysAspLeuArgAsnLysL 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    erGluGluSerMetAsnMetAspSerSerSerValAlaValGluAspVal 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TTACATTGGTGAGTTTGAG.....TATGTCGATGACCACAGAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CCTTCCTCCAAAGTGATTATCAAGTTTCTGATTGTCATGCAGAAGCACGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CTGGCAAGATCGTC.....GTT
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/product= "CDKI"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CDKI from Chenopodium rubrum, Caenorhabditis elegans and Arabidopsis thaliana. CDKI is involved in the cell cycle, and may promote or inhibit cell division and growth. The coding sequence and the protein it encodes are useful in the production of transgenic plants which produce increased or decreased amounts of the CDKI protein, in the identification of herbicides, in genetic and physical mapping and in the isolation of the
                                                                                                                                                                                                   154
                                                                                                                                                                                                                                           557
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4 ValArgArgGluArgAspValValGluGluAsnGlyValThrThrTh
                                                                                                  alAlaGluLysAspLeuArgAsnLysLeuLeuGluCysSerMetLysTyr 187
                                                                                                                                                                                                                                                                                                                                                                                                       AGTTGAAACGTCGACGTGCAATGGTGGTCATGAAATTGAGAGGAGA....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ccrccagrgaaarrccagcgrcrrgcrccagcaacggarccarrggc 427
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     luAspSerSerVal.....SerCysCysSerThr.....SerGluGlu 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TGAACCATCATCCAAGAGAAAGAAGATCAGCAACAGTACTAAC.....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  r.....ThrValLysArgArgLysMetGluGluValAspLeuValG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GTCAGGACACGAGCCCAAGCCGCATTAGCCATGGAAGCTGTTAGTTCTGC
AATTATGATATTGTTAAGGACGTACCGCTG...GAAGGACGCTACGAGTG
                                   AsnPheAspPheGluLysAspGluProLeuGlyGlyGlyArgTyrGluTr 204
                                                                                                                                                                                                 sSerLeuHisGluThrValLysGluAlaGluLeuGluAspPhePheGlnV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CTCGATCAGGACAGGATCAAGCTCTTAGATCTGGAGGTGGAGAGCGCGCA 477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IleValAlaArgAsnSerAlaGlyAlaSerGluThrSerValValIleVa 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     luSerArgIleIleLeuSerProCysValGlnAlaThrAsnArgGlyGly
                                                                                                                                                                                                                                                                               SerSerSerValAlaValGluAspValGluSerArgArgArgLeuArgLy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GGTTCAGCCGGTGTCGCCGGAGATGGTTCAGCAACGCTGCCTGAGCCCTA
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                                                                                                                                                                                                                                                                                                                                                               erTrpIleTyrAspAspLeuAsnLysSerGluGluSerMetAsnMetAsp
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AAA95287;
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DT 17-JAN-2001 (first entry)
XX
Soybean cyclin-dependent kinase in
XX
Soybean; cyclin-dependent kinase in
XX
CDKI; cell growth; herbicide; ss.
XX
OS Glycine max.
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                                                                                                                                                                                                                                                alignment_block:
                                                                                                                                     Align seg 1/1 to: AAA95287
                                                                                                                                                                                                               US-09-574-735C-2 x AAA95287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present sequence is the coding sequence for the soybean cyclin-dependent kinase inhibitor (CDKI). It was isolated by searching a soybean seedling cDNA library for sequences similar to those encoding the CDKI from Chenopodium rubrum, Caenorhabditts elegans and Arabidopsis thaliana. CDKI is involved in the cell cycle, and may promote or inhibit cell division and growth. The coding sequence and the protect in tencodes are useful in the production of transgenic plants which produce increased or decreased amounts of the CDKI protein, in the identification of herbicides, in genetic and physical mapping and in the isolation of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          742
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                                                              129 LysSerGluGluSerMetAsnMetAspSerSerSerValAlaValGluAs 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 620 BP; 191 A; 111 C; 134 G; 183 T; 1 other;
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34 AAAAGTTCCAGCGAGCTTCGAGAGAATTCACAGGAGCCGGAGCCAATGGA 83
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gb_est2:BG873907
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gb_est2:BF983779
gb_est2:BF983779
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gb_est1:AA655401
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9b_est2:BG446151

9b_est1:BE347049

9b_est2:BG841133
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9b_est2:BG823033
9b_htc:AF130081
9b_est1:AI516608
9b_est1:AI516045
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Database length: 1077921985
Search time (sec): 1205.740000
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gb_est2:BF240390
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-Q-/cgn2_1/USPF0_spco1/US9574735/runat_30012002_101838_781/app_query.fasta_1.270
-Q-/cgn2_1/USPF0_spco1/US9574735/runat_30012002_101838_781/app_query.fasta_1.270
-DB=EST -QFMT=fasta_0 -SUFFIX=p2n.rst -GAPOP=12.000 -GAPEXT=4.000
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-DELEXT=7.000 -START=1 -MATRIX=DIOSUM62 -TRANS=100 -THR_MIN=0
-LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MX=100 -THR_MIN=0
-ALIGN=15 -MODE=LOCAL -000TFMT=pfs -NORM=ext -HEAPSIZE=500
-MINLEN=0 -MAXLEN=200000000 -USER=US09574735_@CGN1_1_363
-NCPU=6 -ICPU=3 -LONGLOG -DEV_TIMEOUT=120 -WARR_TIMEOUT=30
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gb_est2:BG831011
gb_est1:AA142274
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AUTHORS
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SOURCE
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US-09-574-735C-2 x BG643706
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LOCUS BG643706
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                                                                                                                                                                                                                                                                                    84 GluGluAspSerSerValSerCysCysSerThrSerGluGluLysSerLy
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                                                                  CCACCAGGGAGAGCACCTTGCAGTTTGATAAGGGATTCAGACAACATT 161
                                                                                                         luThrGluThrSerTrpIleTyrAspAspLeuAsnLysSerGluGluSer
                                                                                                                                                     AAACTTGCTGGAATTT.....GAAGGTAGAAAAAGGA
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Gaps: 4
Percent Identity: 30.952
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EST 24-APR-2001
EST511900 tomato shoot/meristem Lycopersicon esculentum cDNA clone cTOF32G10 5' sequence, mRNA sequence.
BG643706
                                                                                                                                                                                                                                                                                          Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Email: http://www.genome.clemson.edu/orders/index.html.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Lycopersicon esculentum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids I; Solanales; Solanaceae; Solanum;
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EST.
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Generation of ESTs from tomato shoot/meristem tissue
                                                                                                                                                                                                                                                                                                                                                                                              Clemson University Genomics Institute
/note="Vector: pBluescript SK(-); Site_1: EcoR1; Site_2: Xho1; Small expanding leaves from the growing tip were taken from greenhouse plants (4-6wks old TA496). Tissue was immediately frozen in liquid nitrogen."

108 c 144 g 140 t
                                                                                                       /tissue_type="shoot/meristem"
/dev_stage="developing shoots from 4-6wks old plants"
/lab_host="SOLR"
                                                                                                                                                                                             /db_xref="taxon:4081"
/clone="cTOF32G10"
                                                                                                                                                                                                                                        /organism="Lycopersicon esculentum"
/cultivar="TA496"
                                                                                                                                                                       /clone_lib="tomato shoot/meristem"
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i BG831011 602766730F1 NIH_MGC
i AA142274 CK00350.contig CK
i BE798251 601584461F1 NIH_MGC
i BE798064 601582895F1 NIH_MG
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JOURÑAL
COMMENT
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source
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Unpublished (2001)
Contact: Carroll P. Vance
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: vance004@maroon.tc.umn.edu
University of Minnesota name: M381752e TIGR sequence name:
MTCCV34TK More information is available at: http://www.medicago.org
Seq primer: SKmod (CTA 9AA CTA 9tg 9AT CC).
Location/Qualifiers
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Fax: 651-649-5058
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Department of Agronomy and Plant Genetics
University of Minnesota
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barrel medic
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                                                                                216
                                                                    /tissue_type="N2-fixing root nodules"
/dev_stage="effective root nodules harvested one month
/dev_stage="effective root nodules harvested one month
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/lab_host="E. coli strain XLOLR"
/lab_host="E. coli strain XLOLR"
/note="Yector: pBluescript SK-; Site_1: EcoRI; Site_2:
/note="Yector: pBluescript SK-; Site_1: EcoRI; Site_2: PBluescript Sit
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Medicago truncatula"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              /clone_lib="GVN"
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truncatula cDNA clone pGVN-61E20 5' end
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US-09-574-735C-2
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                                                                                                                                                                BG581898 754 bp mrNA EST 11-APR-2001 EST483634 GVN Medicago truncatula cDNA clone pGVN-66M9 5' end, mRNA
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Medicago truncatula
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                                     62 uThrSerValValIleValArg.ArgArgAspSerProProValGluGlu
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GTTCTCCCGGAAAATCCAGGCTTCGT....
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
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post inoculation with Sinorhizobium meliloti"
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BG581998.1 GI:13597062
EST.
                                                                       Email: vance004@maroon.tc.umn.edu
University of Minnesota name: M38306le TIGR sequence name:
MTCDB44TK More information is available at: http://www.med
Seq primer: SKmod (CTA gAA CTA gtg gAT CC).
Location/Qualifiers
                                                                                                                                                                                     411 Borlaug Hall,
Tel: 612 625 5715
Fax: 651-649-5058
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Unpublished (2001)
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolleae
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/cultivar="genotype A17"
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                                                                                                                                                                                                                                St.Paul, MN 55108
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AGAAGAATGAGAATCGTGATGGTGATTTCGCTGTTGAAGGTTCTTTTG
                                                                                                                      AAGTGTCATTCATACCCCTGGTTCAACCACAAGACAAAGGACGAACCACA
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/testage="effective root nodules harvested one month
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/note=""Vector: pBluescript SK-; Site_1: EcoRI; Site_2:
XhOI; cDNA was prepared from polyA+ enriched RNA from
effective root nodules harvested one month post
inoculation with Sinorhizobium meliloti. The cDNA was
directionally ligated into the Uni-ZAP XR vector from
Stratagene and packaged using Gigapack III Gold packaging
extracts. Plasmids containing cDNA inserts were excised
from the recombinant lambda-ZAP phage using Ex-Assist
helper phage and propagated in XLOLR cells."
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84

333

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Percent Similarity:

Ratio:

131.00 1.129 52.018

Gaps: Percent Identity:

223 12 28.251

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REFERENCE
AUTHORS
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alignment_scores:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                source
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Fedorova, M., Pierson, B.L., Samac, D.A., Vance, C.P., Gantt, G.S., Town, C.D., Van Aken, S., Utterback, T., Cho, J. and Fraser, C.M. ESTs from one month old nitrogen-fixing root nodules of Medicago
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          mRNA sequence.
BG582049
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: vance004@maroon.tc.umn.edu
University of Minnesota name: M383113e TIGR sequence name:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        411 Borlaug Hall, 1991 Upper Buford Circle,
Tel: 612 625 5715
Fax: 651-649-5058
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Department of Agronomy and Plant Genetics
University of Minnesota
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EST
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MTCDQ42TK More information is available at: http://www.medicago.org
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                                                                                                            /dev_stage="effective root nodules harvested one month /dev_stage="effective root nodules harvested one month post inoculation with Sinorhizobium meliloti"
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190 c 167 g 209 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                         /clone="pGVN-66H11"
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                                                                                                                                                                                                                                                                                                                                                                                                                   /clone_lib="GVN"
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US-09-574-735C-2 x BG582049

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ACCESSION
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                                                                            SOURCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CCGCCGCCTCCGTAAGGTTCCTCCGCCGCTTCCACCTCGCAAGGAGAGCG
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soybean.
Glycine max
Glycine max
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
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                                                                                                                                       mRNA sequence.
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                                                                                                                                                                       alignment_block:
US-09-574-735C-2 x BE823380/rev
                                                                                                                                                                                                                                                                                                                                                             BASE COUNT
ORIGIN
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          90 .....SerCysCysSerThrSerGluGluLysSerLysArgArgIleG 104
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Align seg 1/1 to reverse of: BE823380
596 GATCAGNACAGGATCAAGNNNNNAGATCTNNNGGTNNNGAGCGCGCAAGT 547
                                                             78 GluGlnCysGlnIleGluGluAspSerSerVal.....
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Other_ESTs: AW471566 corresponding to Gm-c1029-1133 (5') Contact: Vodkin, L.O., PI, A Functional Genomics Program Soybean (NSF 9872565)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ystems.com web site:www.genomesystems.com
Seq primer: 5'-TTTTTTTTTTTTTTTTTT(A/C/G)-3'.
Location/Qualifiers
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Tel: (217) 244-6147
Fax: (217) 333-4582
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/clone="The"library Gm-r1070 is a sequence-driven, reracked set of 9,216 clones selected from cDNA libraries from various tissues and stages of development of soybean that represent 2,639 sequences from immature cotyledons, 1,770 from immature seed coats, 3,938 from flowers, and 869 from young pods. The 5' EST of the source clones from the different libraries was used to select singletons, or a representative of each contig, which were reracked to form library for r1070. The cDNA clones of the reracked Gm-r1070 library were then sequenced at the 3' end. The contig analysis to select unique genes was performed by the laboratory of Ernest Retzel, Center for Computational Genomics and Bioinformatics, University of Minnesota, http://www.cbc.umn.edu/ResearchProjects/Soybean/index.html.

Reracking was performed by Genome Systems, St. Louis, http://www.genomesystems.com, and 3' sequencing by the Keck Center for Comparative and Functional Genomics, University of Illinois, http://www.library.cdu/biotech/keck.html. Note: The corresponding 5' EST from each clone in the Gm-r1070 library is listed in the 'OTHER EST' field. The detailed in the 'OTHER EST' from cach clone can also
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54.286
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be obtained by referring to the Genome Systems clone
the original cDNA library that is also listed under
'OTHER EST'."
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/db_xref="taxon:3847"
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lu...PheValAspLeuGluGluAsnAsnGlyAspAspArgGluThrGlu 119

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GA_Ea0030N24f Gossypium arboreum 7-10 dpa fiber library Gossypium arboreum cDNA clone GA_Ea0030N24f, mRNA sequence.
BG446151
                                                                                                                                                                                                                                                                                                                                                                                                                     Unpublished (2000)
Contact: Wing RA
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Wing, R.A., Frisch, D., Yu, Y., Main, D., Rambo, T., Simmons, J., Henry, D., Wood, T.C., Leslie, A. and Wilkins, T.A. and evolution an integrated analysis of the genetics, development, and evolution of the cotton fiber
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Malvales; Malvaceae; Gossypium.

1 (bases 1 to 896)
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Gossypium arboreum
                                                                                                                                                                                                                                                        Email: rwing@clemson.edu
Seq primer: TAATACGACTCACTATAGGG
High quality sequence stop: 487.
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100 Jordan Hall, Clemson,
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    a
                                                       /clone="GA_Ea0030N24f"
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/tissue_type="Fibers isolated from b
dpa"
/note="Vector: pBK-CMV;
136 c 347 g 1
                                                                                                                                                                               /organism="Gossypium arboreum"
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                                                                                                                                                                                                                                         Location/Qualifiers
                                                                                                                                                             /cultivar="8400"
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BE347049.1 GI:9258902
                                                                                                                                                                                                                          Email: estewatson.wustl.edu
This clone is available through: Genome Systems, Inc. 4633 World
Parkway Circle St. Louis, Missouri 63134 For further information
call: (800) 430-0030 or (314) 427-3222 FAX:(888) 919-3324 or (314)
427-3324 or contact: clones@genomesystems.com or
info@genomesystems.com web site: www.genomesystems.com
Insert Length: 1181 Std Error: 0.00
                                                                                                                                                                                                                                                                                                                                                                                                                                        4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Shoemaker R/Public Soybean EST Project
Public Soybean EST Project
Washington University School of Medicine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Unpublished (1999)
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Fax: 314 286 1810
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3.026
79.167
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pT7T3Pac (Pharmacia);
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2
47.917
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       Site_1: EcoRI;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Beck, C.,
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VERSION
KEYWORDS
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LOCUS BG841133
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US-09-574-735C-2 x BE347049
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                                                                                                                                                                                                  ACCESSION
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                                                                                                                                                                                                                                                                                                                                                                                                                           195 uProLeuGlyGlyGlyArgTyrGluTrp 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    441
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                162 luAlaGluLeuGluAspPhePheGlnValAlaGluLysAspLeuArgAsn 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1,30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      391 CCAGCCTCAATTTCAAATCGTTCAGTTTGTTGAGTGAGTTTTCCGGAGAC 440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             120 hrSerTrpIleTyrAspAspLeuAsn.....Lys 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   344 GCCG...TCAGATCTGCAGACCAAGGGTTTCGAAACGGTAGAAGACTCAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  145 pValGluSerArgArgArgLeuArgLysSerLeuHisGluThrValLysG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     103 eGluPheValAspLeuGluGluAsnAsnGlyAspAspArgGluThrGluT 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TCGGAGGAATCGGCGATGATTCCGGCGAAGTCTTCCGCGGCGGTGCTGAN 490
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CCGTTCACAGAG.....AAGTACAACTTTGATATTGTTAGAGATTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LysLeuLeuGluCysSerMetLysTyrAsnPheAspPheGluLysAspGl 195
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                                                                                                                                                                                                                                                                                                                                                                                                  GCCGTTG...GAGGGTCGCTACCAGTGG 623
                       Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade; Panicoideae; Andropogoneae; Zea.
                                                                                                                                                                                                                                                MEST18-A04.T3 ISUM4-TN
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                                                                                               Zea mays
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                                                                                                                         lea mays.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        cells (Gibco BRL). This library was constructed by Dr. Randy Shoemaker."

158 c 145 g 147 t 3 others
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to 604)
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Gaps: 6
Percent Identity: 33.333
                                                                                                                                                                                                                                              mRNA EST 29-MAY-2001
Zea mays cDNA clone MEST18-A04 3', mRNA
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ACCESSION
VERSION
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LOCUS AT728644
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US-09-574-735C-2 x BG841133/rev
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ORIGIN
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                                                                                DEFINITION
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TITLE
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                                                                                                                                                                                                                                          197 euGlyGlyArgTyrGluTrpValLysLeuAsnPro 209
                                                                                                                                                                                                                                                                                                                      180 uLeuGluCysSerMetLysTyrAsnPheAspPheGluLysAspGluProL 197
                                                                                                                                                                                                                                                                                                                                                                 164 GluLeuGluAspPhePheGlnValAlaGluLysAspLeuArgAsnLysLe 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  source
                                                                                                                                                                                                                                                                                  TGGACGGCCGGTACGAGTGGGTCCGAGTGCGGCCC
              BNIGH111291 Six-day Cotton fiber Gossypium hirsutum cDNA to (AJ002173) cyclin-dependent kinase inhibitor protein (Chenopodium rubrum), mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Unpublished (2001)
On May 25, 2001 this sequence version replaced gi:14207455.
Contact: Patrick S. Schnable
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Tel: 515-294-0975
Fax: 515-294-2299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Qiu, F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     G405 Agronomy,
AI728644.1 GI:5047496
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: schnable@iastate.edu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      resulting DNA:RNA hybrid was treated with RNase H and used as a template for DNA Poll-catalyzed second strand synthesis. After the addition of EcoRI adaptors, the ds-cDNAs were digested with NotI and size-selected. The resulting molecules were directionally cloned into the EcoRI and NotI sites of the pT713PAC vector. The library then went through one round of normalization to CoT value of 5 based on the methods of Marcelo Bento Soares (Genome Research 6: 791-806, 1996)."
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3.243
76.087
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/clone="MEST18-A04"
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/tissue_type="Seedling and silk"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Zea mays"
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Gaps: 1
Percent Identity: 43.478
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CCT CAC TAA AG)
(ATT AAC CCT CAC TAA AG).
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KEYWORDS
SOURCE
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US-09-574-735C-2 x AI728644
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                                                                                        GCTTTCCGGAGATATGTGTTCCGGT.....
                                                                                                                                                                                                                                                  eValAlaArgAsnSerAlaGlyAlaSerGluThrSerValValIleValA 69
                                                                                                                                                                                                                                                                                       TCGCTGAACAAGCCTATTTACTTAGCTACTTCCTCGGGTTCTTGTGGAGT
                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTATCAAAGAGAAAAACTGTTGGTTCTCGAGAATTGCAAGAATTAG 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAACGAAGTGCAGAAGCAGCTGAAATGGAAGCTTCAAGCACGAGCTTCTC
                                                                      AATTCATCGGCTTCTCGTTCTTCGAGCAACGAGTCGTGGTGATATTCTCAA
                                                                                                                                                                          rgArgArgAspSerProProValGluGluGlnCysGlnIleGluGluGlu 85
Blewitt,M., Matz,E.C., Davy,D.F. and Burr,B. ESTs from developing cotton fiber Unpublished (1999)
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upland cotton.

upland cotton.

Gossypium hirsutum

Gossypium hirsutum

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Eukaryota; Vagnoliophyta; eudicotyledons; core eudicots;

Spermatophyta; Magnoliophyta; eudicotyledons; Gossypium.

Rosidae; euroids II; Malvales; Malvaceae; Gossypium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Biology Department
Brookhaven National Laboratory
Upton, NY 11973, USA
Tel: 516-344-3396
Fax: 516-344-3407
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Ben Burr
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       burr@bnlux1.bnl.gov
imer: T3 Primer.
                                                                                                                                                                                                                                                                                                                                                                                             ....GluValAspLeuValGluSerArgIleIleLeuSer
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/lab_host="XL1-Blue"
/note="Vector: pBluescript II KS+"
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0.941
52.212
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|cultivar="Acala Maxxa"
|db_xref="taxon:3635"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /clone_lib="Six-day Cotton fiber"
/tissue_type="immature fiber"
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SOURCE
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                                                                                                                                                                                                                                                                                                                                                                            was cloned directionally, not all sequences generated with primer were from the 5' end (same with forward primer and 3 Average inset size is >2.2 kb plate: 169 row: A column: 02
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cereal Research Centre, Agriculture and Agri-food Canada 195 Dafoe Rd, Winnipeg, MB, Canada R3T 2M9 Tel: (204) 983-2340 Fax: (204) 983-6004 Email: Scloutier@em.agr.ca
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooldea
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Contact: Dr. Sylvie Cloutier
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/note="vector: Lambda ZapII; mass excised in plasmid
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mRNA obtained from wheat NIL Thatcher Lr1 24 hours after
inoculation with leaf rust pathogen Puccinia triticina
race BBB carrying the avirulence gene Avr1."
a 216 c 231 g 103 t
                                                                                                                                                                                                                                                   /organism="Triticum aestivum"
/cultivar="Thatcher Lr1"
/db_xref="taxon:4565"
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                                                                                                           602494996F1 NIH_MGC_75 Homo sapiens cDNA clone IMAGE:4609007 5',
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Homo sapiens
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103 IleGluPheValAspLeuGluGluAsnAsnGlyAspAspArgGluThrGl 119
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Tissue Procurement: CLONTECH Laboratories, Inc
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National Institutes of Health, Mammalian Gene Collection (MGC)
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Roest-Crollius, H., Jaillon, O., Dasilva, C., Bouneau, L., Fisher, C., Bernot, A., Fizames, C., Wincker, P., Brottier, P., Quetier, F., Saurin, W. and Weissenbach, J.
Human gene number estimate provided by genome wide analysis usin Tetraodon nigroviridis DNA sequence
Unpublished
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Tetraodon nigroviridis genome survey sequence PUC-Ori end of clone
156C05 of library G from Tetraodon nigroviridis, genomic survey
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Roest-Crollius, H., Jaillon, O., Dasilva, C., Fizames, C., Fisher. Bouneau, L., Billault, A., Quetier, F., Saurin, W., Bernot, A. and Weissenbach, J.
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                                    Unpublished (1996)
Contact: Marra M/Mouse EST Project
Contact: Marra M/Mouse EST Project
WashU-HHMI Mouse EST Project
WashIngton University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Lo
Tel: 314 286 1810
Fax: 314 286 1810
                                                                                                                                                                                                                 Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dub
Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.
Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
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This clone is
                 Email: mouseest@watson.wustl.edu
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                                                                                    ysSerGluGluSerMetAsnMetAspSerSerSerValAlaValGluAsp 145
                                                                                                                                                          nGlyAspAspArgGluThrGluThrSerTrpIleTyrAspAspLeuAsnL 129
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              primer: -28m13 rev1 ET from Amersham h quality sequence stop: 411.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  വ
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1.059
54.595
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Mus musculus"
/strain="NIH/Swiss"
/db_xref="taxon:10090"
/clone="IMAGE:1211235"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /sex="pooled"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /clone_lib="Stratagene mouse heart (#937316)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length: 185
Gaps: 10
Percent Identity: 23.784
                                                   .ACCAGCGCCCACCTGGAG...
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                  162
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                                                     366
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alignment_block:
US-09-574-735C-2 x BH139743/rev
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KEYWORDS
                                                                                                                                                                                                                     alignment_scores:
Quality:
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LOCUS BH139743
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                                                                                                                                                                                                                                                                                                                                                                                          BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FEATURES
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                                                                                                                                  Percent Similarity:
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TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   JOURNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              162 uAlaGlu.....LeuGluAspPhePheGlnValAlaGluLysAspLeuA 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         367
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           High quality sequence start: 22
High quality sequence stop: 792
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Unpublished (2001)
Contact: Brendan J Loftus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 (bases 1 to 941)
Loftus,B., Wang,Z., Van Aken,S. and Fraser,C.
Loftus,B., Wang,Z., Van Aken,S. and Loftus,B., Wang,Z.
Loftus,B., Wang,Z., Van Aken,S. and Loftus,B.
Loftus,B., Wang,Z., Van Aken,S. and Loftus,B.
Loftus,B., Wang,Z., Van Aken,S. and Loft
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BH139743.1 GI:15098804
GSS.
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BH139743
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Class: shotgun
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Seq primer: M13-Forward
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DNA library
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: enta@tigr.org
Clones are derived from the Entamoeba histolytica HM1:IMSS sheared
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Tel: 301 838 0200
Fax: 301 838 0208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Entamoeba histolytica.
Entamoeba histolytica
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                                                                                                                                                                         Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                /db_xref="taxon:5759"
/db_xref="taxon:5759"
/clone_lib="Entamoeba histolytica Sheared DNA"
/note="Vector: pHOS1; Site_1: Bst I; Constructed at The
Institute for Genomic Research (TICR), Rockville, MD.
Genomic DNA isolated from broth cultures of E. histolytica
using a method described by Clark and Diamond (Clark,
C.G., and Diamond, L.S. (193) Entamoeba histolytica: a
method for isolate identification. Exp. Parasitol.
77:450.). The DNA was mechanically sheared to give a
tight size distribution (-2 kb). The v + i method used for
the library construction is described in detail in Smith,
H.O. and Venter, J.C. (Making small insert libraries for
whole genome shotgun sequencing projects. In Genome
Sequencing: A Practical Approach, eds. M. Vaudin and B.
Barell, Oxford University Press, 1999)."
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                                                                                                                                  107.00
0.991
54.545
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/strain="HM1:IMSS"
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                                                                                                    Length: 198
Gaps: 9
Percent Identity: 23.737
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Align seg 1/1 to reverse of: BH139743

from:

. 6

	180 euLeuGluCysSerMetLysTyrAsnPheAspPheGluLysAsp 194 ::: :::	
180 513	163 aGluLeuGluAspPhePheGlnValAlaGluLysAspLeuArgAsnLysL ::::::::::::::::::::::::::::::::::	
163 563	147 GluSerArgArgArgLeuArgLysSerLeuHlsGluThrValLysGluAl:::::::::::::::::::::::::::::::::::	
146 607	130 erGluGluSerMetAsnMetAspSerSerSerValAlaValGluAspVal :: :::::: 638 AACTAGAAGACATTAAAATGGAT	
130 639	115 pargGluThrGluThrSerTrpIleTyrAspAspLeuAsnLysS :::	
115 689	101 ArgArgIleGluPheValAspLeuGluGluAsnAsnGlyAspAs :::	- 1 - 1-4
100 739	84 luGluAspSerSerValSerCysCysSerThrSerGluGluLysSerLys	-1
84 789		~
823		m
67	51 GlyIleValAlaArgAsnSerAlaGlyAlaSerGluThrSerValValIl	
50 823		m
34 855	17 IThrThrThrThrValLysArgArgLysMetGluGluGluValAspLeuV : ::::: :::::::: : 885AAAGAAAAATGAATAAAAAATGCATATTGA	œ
17 886	1 MetAlaAlaValArgArgArgGluArgAspValValGluGluAsnGlyVa :	9

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/cgn2_6/ptodata/2/ina/6A_COMB.seq:US-08-374-077C-1 + 98.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Search information block:
Query: US-09-574-735C-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OM of: US-09-574-735C-2 to: Issued_Patents_NA:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Database sequences: 351203
Database length: 113238999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Database:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Results were produced by the GenCore software, Copyright (c) 1993-2000 Compugen Ltd.
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equences: 351203
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alignment_block:
US-09-574-735C-2 x US-07-667-276A-3
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                                                                                        alignment_scores:
Quality:
                                                                                                                                                                US-07-667-276A-3
                                                      Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 3, Application Patent No. 5470971
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: 215-875-8394 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                    FRAGMENT TYPE:
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                        HYPOTHETICAL: I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
LENGTH: 2017 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER: 37
TELECOMMUNICATION INFORMATION: 215-875-8383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                          FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                 OTHER INFORMATION:
OTHER INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Weiser, Gerard REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: FILING DATE: 11-MAR
                                                                                                                                                                                                                                                                                        NAME/KEY: CDS
LOCATION: 484..1725
                                                                                                                                                                                                                                                                                                                                                                   ORGANISM:
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                                                                                                                                                                                                                                                                                                                                              STRAIN: S288C
                                                                                                                                                                                                                                                      NAME/KEY: misc_feature
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                                                                       Ratio:
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                                                        Percent Identity:
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seq_name: /cgn2_6/ptodata/2/ina/5A_COMB.seq:US-07-667-276A-3
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/cgn2_6/ptodata/2/ina/5A_COMB.seq:US-08-676-974-5
/cgn2_6/ptodata/2/ina/5B_COMB.seq:US-09-098-487-4
/cgn2_6/ptodata/2/ina/5B_COMB.seq:US-09-098-887-5
/cgn2_6/ptodata/2/ina/5A_COMB.seq:US-08-676-967-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: INOUYE, MASAYOTI
TITLE OF INVENTION: STRESS-INDUCED PROTEINS, GENES CODING
TITLE OF INVENTION: THEREFOR, TRANSFORMED CELLS OF ORGANISMS, METHODS AND
TITLE OF INVENTION: APPLICATIONS
                                                                                                           /note= "Base #1 of Sequence No.
corresponds to base -483 of the
Figure 11 of the application"
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alignment_block: us-09-574-735C-2 \times us-08-533-306A-5
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INFORMATION FOR SEQ ID NO: 55
SEQUENCE CHARACTERISTICS:
LENGTH: 2680 base pairs
TYPE: nucleic acid
TYPE: Achil
                                                                                                                                                        1093 TCCCTGGCTCGG......GCCCTTGAAGAGGCCTTGGAAGCCAA 1130
                                                                                                                                                                                                                                                                                                                        1005 AGCCGAGGAGAAAAACATCTCTTCCAAATACGCGGATGAGAGGGACAGAG
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NAME: Smith, DeAnn F.
REGISTRATION NUMBER: 36683
REFERENCE/DOCKET NUMBER: 21
TELECOMMUNICATION INFORMATION:
1181 TGGTCAGCTCCAAGGATGACGTGGGCAAGAACGTCCATGAGCTGGAGAAG 1230
                                                                                                                                                                                                                                     1055 CTGAGGCAGAAGCCAGGGAG.....AAGGAAACCAAGGCCCTG 1092
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INDIVIDUAL ISOLATE: Sample 2
TISSUE TYPE: Acute myelomonocytic leukemia,
TISSUE TYPE: subtype (inv16)
POSITION IN GENOME:
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                                                                                                                   83 uGluGluAspSerSerValSerCysCysSerThrSerGlu......
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                                                                                                                                                                                                                                                                            50 lyGlyIleValAlaArgAsnSerAlaGlyAlaSerGluThrSerValVal 66
                                                                                                                                                                                                                                                                                                                                                           33 uValGluSerArgIleIleLeuSerProCysValGlnAlaThrAsnArgG 50
                                                                                                                                                                                                                                                                                                                                                                                                                                     17 ValThrThrThrThrValLysArgArgLysMetGluGluValAspLe 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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CLASSIFICATION:
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                                                                                                                                                                                            IleValArgArgArgAspSerProProValGluGluGlnCysGlnIleGl 83
                                                                            AGAGGAACTCGAGCGGACCAACAAAATGCTCAAAGCCGAAATGGAAGACC 1180
                            Quality:
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310) 641-0270
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seq_documentation_block:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 5,
Patent No. 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
               TELEFAX: (810) 641-0270 INFORMATION FOR SEQ ID NO: 5: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1363 GAAAGGGATCTCCAAGCCCGGGACGAGCAGAATGAGGAGAAGAGGAGGCA
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                                                                                                                                                                                                                                                                    COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   195 uProLeuGlyGlyArgTyrGluTrpValLys 206
                                                                             REFERENCE/DOCKET NUMBER: 21
TELECOMMUNICATION INFORMATION:
TELEPHONE: (810) 641-1600
                                                                                                                                            ATTORNEY/AGENT INFORMATION:
NAME: Smith, Deann F.
REGISTRATION NUMBER: 36683
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                            APPLICATION NUMBER:
-FILING DATE: NO. 58
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                           ZIP: 48303
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ENGTH:
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5869611
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Collins, Francis S.
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                                                                                                                                                                                                                            5869611ember
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alignment_block:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-09-574-735C-2 x US-08-742-923A-5
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                                                                                                                                                                                                                                1313
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HYPOTHETICAL: N
ANTI-SENSE: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1181 TGGTCAGCTCCAAGGATGACGTGGGCAAGAACGTCCATGAGCTGGAGAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1093 TCCCTGGCTCGG......GCCCTTGAAGAGGCCTTGGAAGCCAA 1130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1005 AGCCGAGGAGAAAAACATCTCTTCCAAATACGCGGATGAGAGGGACAGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TISSUE TYPE: Acute myelomonocytic leukemia, M4EO TISSUE TYPE: subtype (invl6) POSITION IN GENOME:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      961 GTGTCCAACCTGGAAAAGAAGCAGAGGAAATTTGATCAGTTG.....TT 1004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          83 uGluGluAspSerSerValSerCysCysSerThrSerGlu.....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   17 ValThrThrThrValLysArgArgLysMetGluGluValAspLe 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY:
LOCATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Homo sapiens INDIVIDUAL ISOLATE: Sar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRANDEDNESS:
TOPOLOGY: lin
hePheGlnValAlaGluLysAspLeuArg......Asn 178
                                                                                      gLeuArgLysSerLeuHisGluThrValLysGluAlaGluLeuGluAspP 168
                                                                                                                                     GAAAGGGATCTCCAAGCCCGGGACGAGCAGCAGAATGAGGAGAAGAGGAGGCA 1412
                                                                                                                                                                                                                                ACGCCAAACTGCGGCTGGAAGTCAACATGCAGGCGCTCAAGGGCCAGTTC 1362
                                                                                                                                                                                                                                                                                                                      .ATGAAGACGCAGCTGGAAGAGCTGGAGGACGAGCTGCAAGCCTCGGAGG
                                                                                                                                                                                                                                                                                                                                                pArgGluThrGluThrSerTrpIleTyrAspAspLeuAsnLysSerGluG 132
                                                                                                                                                                                                                                                                                                                                                                                                                 TCCAAGCGGCCCTGGAG...ACCCAGATGGAGGAG...
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CTGAGGCAGAAGCCAGGGAG.....AAGGAAACCAAGGCCCTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        uValGluSerArgIleIleLeuSerProCysValGlnAlaThrAsnArgG 50
                                                                                                                                                                                                                                                                      luSer......metAsnMet.....
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AGAGGAACTCGAGCGGACCAACAAATGCTCAAAGCCGAAATGGAAGACC 1180
                                                                                                                                                                              .....AspSerSerSerValAlaValGluAspValGluSerArgArgAr 151
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sample 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .....GluLys 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1230
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seq_documentation_block:
                                                                                                                    ; LOCATION:
US-08-533-306A-3
                                                                  alignment_scores:
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                Ratio:
Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 3, Application US/08533306A Patent No. 5837457
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                     TOPOLOGE
MOLECULE TYPE: CUN
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1456
                                                                                                                                                                                                                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO: 3: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1492 AAGAAGCTGGAAGGGGACCTGAAA...GACCTGGAGCTTCAGGCCGACTC 1538
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APPLICANT:
                                                                                                                                                                                                 ORGANISM: Homo sapiens
INDIVIDUAL ISOLATE: Sample 1
TISSUE TYPE: Acute myelomonocytic leukemia, M4Eo
TISSUE TYPE: subtype (lnv16)
POSITION IN GENOME:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOCTWARE: PatentIn Release #1.0, Version CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ZIP: 48303
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            195 uProLeuGlyGlyArgTyrGluTrpValLys
                                                                                                                                                                      FEATURE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: 21
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
NAME: Smith, Deann F.
REGISTRATION NUMBER: 366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT:
                                                                                                                                                                                                                                                                                          ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER:
FILING DATE: Septem
CLASSIFICATION: 439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STREET: P.O. Box 828
CITY: Bloomfield Hills
                                                                                                                                                                                      CHROMOSOME/SEGMENT:
                                                                                                                                                                                                                                                                                                                                                                           STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                LENGIH: 2887 base pairs TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEPHONE:
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                                                                                                                                                      NAME/KEY:
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Collins, Francis S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (810)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Siciliano, Michael J.
                                                                                                                                                                                                                                                                                                                                                              linear
                                                                                                                                    1..2658
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (810) 641-1600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Floppy disk
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              100.50
0.838
52.632
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                                                                                                                                                                                    16[inv(16)(p13q22)]
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vaps: 13
Percent Identity: 25.439
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alignment_block:
US-09-574-735C-2 x US-08-533-306A-3
                                                                                                                                                                                                                       seq_documentation_block:
                                                                                                                                                                                                                                                                       seq_name: /cgn2_6/ptodata/2/ina/5B_COMB.seq:US-08-742-923A-3
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                                                                                                                                                              Sequence 3, Application US/08742923A Patent No. 5869611
                                                                                                                                             GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1663
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APPLICANT: Liu, Pu
APPLICANT: Collins, Francis S.
APPLICANT: Siciliano, Michael J.
APPLICANT: Claxton, David
TITLE OF INVENTION: Markers for I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        132 luSer...... 136
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ACTGCAGAGACAGCTTCACGAG.....TATGAGACGGAACTGGAAGAC. 1662
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GANAGGGATCTCCAAGCCCGGGACGAGCAGCAGTGAGGAGGAGGAGGCA 1619
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              pArgGluThrGluThrSerTrpIleTyrAspAspLeuAsnLysSerGluG 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AGAGGAACTCGAGCGGACCAACAAAATGCTCAAAGCCGAAATGGAAGACC 1387
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CTGAGGCAGAAGCCAGGGAG.....AAGGAAACCAAGGCCCTG
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                                                                                                                                                                                                                                                                                                                                                                                uProLeuGlyGlyGlyArgTyrGluTrpValLys
                                                                                                                                                                                                                                                                                                                                                                                                                                         AAGAAGCTGGAAGGGGACCTGAAA...GACCTGGAGCTTCAGGCCGACTC 1745
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TCCAAGCGGGCCCTGGAG...ACCCAGATGGAGGAG.....
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            uGluGluAspSerSerValSerCysCysSerThrSerGlu.....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LysLeuLeuGluCysSerMetLysTyrAsnPheAspPheGluLysAspGl 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        hePheGlnValAlaGluLysAspLeuArg......Asn 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ACGCCAAACTGCGGCTGGAAGTCAACATGCAGGCGCTCAAGGGCCAGTTC 1569
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .ATGAAGACGCAGCTGGAAGAGCTGGAGGACGAGCTGCAAGCCTCGGAGG 1519
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ......GluLys 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .....GAGCGAAACGAACGTGCCCTGGCAGCTGCAGCAAAG 1698
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .....AspSerSerSerValAlaValGluAspValGluSerArgArgAr 151
        Markers for Detection of Chromosome
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TITLE OF INVENTION:

Rearrangements

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alignment_scores:
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                                                                                                                                                                                                                                                                                                                                                                  US-09-574-735C-2 x US-08-742-923A-3
                                                                                                                                                                                                                                                                                                                                                                                                                              Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Smith, DeAnn F.
REGISTRATION NUMBER: 36683
REFERENCE/DOCKET NUMBER: 2115
TELECOMMUNICATION INFORMATION:
TELEPHONE: (810) 641-1600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: (810) 641-0270 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                           1168 GTGTCCAACCTGGAAAAGAAGCAGAGGAAATTTGATCAGTTG.....TT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              * TOPOLOGY: linear MOLECULE TYPE: CDNA HYDOTHETICAL: NO
1300 TCCCTGGCTCGG.......GCCCTTGAAGAGGCCCTTGGAAGCCAA 1337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE TYPE: Acute myelomonocytic leukemia, M4EO TISSUE TYPE: subtype (inv16) POSITION IN GENOME:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
LENGTH: 2887 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/742,923A
FILING DATE: No. 5869611ember 1, 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DRIGINAL SOURCE:
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                                                                                                                                                                                                   33 uValGluSerArgIleIleLeuSerProCysValGlnAlaThrAsnArgG 50
                                                                                                                                                                                                                                                                                 17 ValThrThrThrValLysArgArgLysMetGluGluValAspLe 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Homo sapiens INDIVIDUAL ISOLATE: Sar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CHROMOSOME/SEGMENT: 16[inv(16)(p13q22)]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LOCATION:
                                    IleValArgArgArgAspSerProProValGluGluGlnCysGlnIleG1 83
                                                                                                                                                             AGCCGAGGAGAAAAACATCTCTTCCAAATACGCGGATGAGAGGGACAGAG
                                                                                                                  lyGlyIleValAlaArgAsnSerAlaGlyAlaSerGluThrSerValVal 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Quality:
Ratio:
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O. Box 828
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; FEATURE:
; NAME/KEY: CDS
; LOCATION: 58..2319
US-09-214-564A-5
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                                                                                                                                                                                                SEQ ID NO 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 5, Application US/09214564A Patent No. 6150515
                                                                                                                                                                                                                                                                                                                       APPLICANT: Sharp, Phillip A.
APPLICANT: Zhou, Qiang
TITLE ORINVENTION: TAT-SF: Cofactor For Stimulation Of Transcriptional
TITLE OF INVENTION: Elongation By HIV-1 TAT
TILE OF INVENTION: Elongation By HIV-1 TAT
TILE REFERENCE: M656/7042
CURRENT APPLICATION NUMBER: US/09/214,564A
CURRENT FILING DATE: 1999-08-18
PRIOR APPLICATION NUMBER: US 60/021,218
PRIOR PILING DATE: 1996-07-03
PRIOR PILING DATE: 1996-12-13
PRIOR PILING DATE: 1996-12-13
PRIOR PILING DATE: 1996-12-13
PRIOR PILING DATE: 1996-12-13
                                                                                                                                                                                                                     NUMBER OF SEQ ID NOS:
SOFTWARE: FastSEQ fo
                                                                                                                                                                                                                                                                        PRIOR APPLICATION NUMBER: PCT
                                                                                                       LENGTH: 2672
TYPE: DNA
ORGANISM: Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TCCAAGCGGGCCCTGGAG...ACCCAGATGGAGGAG......
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               hePheGlnValAlaGluLysAspLeuArg......Asn 178
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alignment_scores: Quality:

100.00

Length:

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Patent NC. CALLER GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Sharp, Phillip A.
APPLICANT: Shou, Qiang
TITLE OF INVENTION: TAT-SF: Cofactor For Stimulation Of Transcriptional
TITLE OF INVENTION: Elongation By HIV-1 TAT
FILE REFERENCE: M0656/7042
CURRENT APPLICATION NUMBER: US/09/214,564A
                                                                                                                                                                                                                                                                                                                    seq_documentation_block:
                                                                                                                                                                                                                                                                                                                                                                    seq_name: /cgn2_6/ptodata/2/ina/6A_COMB.seq:US-09-214-564A-1
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Percent Similarity:
                                                                                                                                                                                                                                                               Sequence 1, Application US/09214564A Patent No. 6150515
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      104 GluPheValAspLeuGluGluAsnAsnGlyAspAspArgGluThrGluTh 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ..SerGluGluSerMetAsnMetAspSerSerSerValAlaValGluAsp 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AGGGTTTGAAGGCAGCTGCTCCCAAAAAGAGTCTGAAGAAGGCAATCCCG 1525
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GluGlnCysGlnIleGluGluAspSerSerValSerCys.....
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                                                                                                                                                                                                                                                                                                                                                                                                                    .....AACTCCGAATTTGAAGATGAC 1869
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AA.....AATGTTCTTGACAAAGAGTTAGAAGAAAATGACTCTGAA... 1848
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TGGTCTCGAGAAAGATTTGGACGAGGAAGGTTCTGAAAAGGAGCTTCATG 1807
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ValGluSerArgArgArg..... 151
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .....GATGACCTCAACAAGGAGTCTGAAGAGGAGGTTGGCC 1657
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CTCAAAAATGATTGTGAAGAG...AATGGCCTTGCAAAGGAATCTGAA.. 1620
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TAAGAGGATCTGAAGAGGATAGTCCTAAAAAAGAGTCTAAAAAAGAAGACA 1575
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ......GluLysSerLysArgArgIle 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GCTGAAGAAGGCTGCCCTGAAAAAGAATCTGAAGAGGGCTGCCCCAAAAG 1475
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CTGAAAACAATGCT.....AAGGAAAGTAGCCCCGAAAAAGAG 1425
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Percent Identity: 26.066
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; NAME/KEY: unsure
; LOCATION: 2731..2731
; OTHER INFORMATION: n =
US-09-214-564A-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: FastSEQ for Windows Version SEQ ID NO 1
LENGTH: 2815
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PRIOR FILING DATE: 1996-07-03
PRIOR APPLICATION NUMBER: US 60/03,152
PRIOR FILING DATE: 1996-12-13
PRIOR APPLICATION NUMBER: PCT/US97/11713
PRIOR FILING DATE: 1997-07-03
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LOCATION: 46..46
OTHER INFORMATION: n
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LOCATION:
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TGCTCTGAAAAACAGTCTGAAGATGGCTCCGAAAGAGAATTTGAAGAAAA 1809
                                 ValGluSerArgArg.....
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                                                                                                                      ..SerGluGluSerMetAsnMetAspSerSerSerValAlaValGluAsp 145
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seq_documentation_block:
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                                                                                          Align seg 1/1 to: US-08-374-077C-1
                                                                                                                                                                                US-09-574-735C-2 x US-08-374-077C-1
                                                                                                                                                                                                                                                                                                              Percent Similarity:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
LENGTH: 8075 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
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CORRESPONDENCE BURNS, DOANE, SWECKER & MATHIS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    184 SerMetLysTyrAsnPheAspPheGluLysAsp 194
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FEATURE:
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ITTLE OF INVENTION: Calcium Channel Subunit
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LOCATION:
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STRANDEDNESS: SILL
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1 MetAlaAlaValArgArgArgGluArgAspValValGluGluAsnGlyVa
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Ren, Dejian
Zheng, Wei
Dubald, Manuel Marcel Paul
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seq_documentation_block:
; Sequence 1, Application US/08895590
; Patent No. 6207410
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        112 nGlyAspAspArgGluThrGluThrSerTrpIleTyrAspAspLeuAsnL 129
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                129 ysSerGluGluSerMetAsn.....MetAspSerSerSerValAla 142
                                                                                                                                                                                CORRESPONDENCE ADDRESS:
ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS, LLP
STREET: 699 Prince Street
                                                                                                                                                                                                                                                                     APPLICANT: Dubald, Manuel Marcel Paul TITLE OF INVENTION: Genes Encoding an Insect Calcium Channel NUMBER OF SEQUENCES: 101
                                                                                                                                                                                                                                                                                                                                                  APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                             APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            79
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 96 GluGluLysSerLysArgArgIleGluPheValAspLeuGluGluAsnAs 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            64 rValValIleValArgArg.....ArgAspSerProProValGluGluG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       48 AsnArgGlyGlyIleValAlaArgAsnSerAlaGlyAlaSerGluThrSe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             17 lThr.....ThrThrThrValLysArgArgLysMetGluGluGluV
                                                                                                                                                       STREET: 699 Film
CITY: Alexandria
                                                                               COUNTRY: USA
ZIP: 22314-3187
                                                                                                                                         STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LysAspGluProLeuGlyGlyGly 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              euArgAsnLysLeuLeuGluCysSerMetLysTyrAsnPheAspPheGlu 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTGATGAGCAGGAACAGCAGCACGACCAAGGTGATTCCGCTGAAGAGGA 1502
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                                                                                                                                         ٧A
                                                                                                                                                                                                                                                                                                                         Zheng, Wei
Dubald, Manuel Marcel Paul
                                                                                                                                                                                                                                                                                                                                                                     Hall, Linda
Ren, Dejian
                                                                                                                                                                                                                                                                                                                                                                                                      Linda M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ....TACGGTGATTTCGATC 1402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1166
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alignment_scores:
Quality:
Ratio:
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; LOCATION:
US-08-895-590-1
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                                                                                                                         1363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1117 GTAGCGGCAGTTGCGGCAGCAGCAGCAACAGGCCCAGGAGCAATCGCT 1166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE: 19-JAN-1995
ATTORNEY/AGENT INFORMATION:
NAME: McGowan, Malcolm M.
REGISTRATION NUMBER: 39,300
REFERENCE/DOCKET NUMBER: 0226
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                        1290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: 703-836-2021 INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                      1249
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129 ysSerGluGluSerMetAsn...
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SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                         48
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                                                                                                                                                                 96
                                                                                                                                                                                                                                          79 lnCysGlnIleGluGluAspSerSerValSerCysCysSerThrSer 95
                                                                                                                                                                                                                                                                                                                     64 rValValIleValArgArg.....ArgAspSerProProValGluGluG 79
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 MetAlaAlaValArgArgGluArgAspValValGluGluAsnGlyVa 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRANDEDNESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER:
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                                 CGCGGAC.....
                                                                                                                                                                                                                                                                                  CGACGTTGTCGTGAGAAAGAACTCAAGGAATCGTCCCTCGATCAGAAGGA 1339
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   alAspLeuValGluSerArgIleIleLeuSerProCysValGlnAlaThr 47
                                                                             nGlyAspAspArgGluThrGluThrSerTrpIleTyrAspAspLeuAsnL 129
                                                                                                                                                             GluGluLysSerLysArgArgIleGluPheValAspLeuGluGluAsnAs 112
                                                                                                                                                                                                                                                                                                                                                                 AACGACTCA.....CTCGAAGACGTTGGCGAGGTGGACGACAACGC 1289
                                                                                                                                                                                                                                                                                                                                                                                                     AsnArgGlyGlyIleValAlaArgAsnSerAlaGlyAlaSerGluThrSe 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                lThr.....ThrThrThrValLysArgArgLysMetGluGluV 31
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157..7704
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0.891
52.885
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.....MetAspSerSerSerValAla 142
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                                         .....TACGGTGATTTCGATC 1402
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                                                                                                                       GACGACGAGGACGAGAA 1379
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alignment_scores:
   Quality:
                                                                                                                                   ; TOPOLOGY: US-08-668-128B-7
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; Sequence 7, Applicatio
; Patent No. 5840568
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               seq_name:
    Percent Similarity:
                                                                                                                                                                                                                                                                    TELEFAX: (212) 838-38 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1591 CTAATTGATAATTTTGGTGGCGGT 1614
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILLING DATA:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/580,980
FTT.ING DATE: 03-JANUARY-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/668,128B
FILING DATE: 21-JUNE-1996
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1503 AGACCACGACGAGGACGTCGACGAGTACTTTGAGGAGGAGGAGGACGACA 1552
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                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
LENGTH: 2085 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                       FILING DATE: 07-JUNE-1995
ATTORNEY/AGENT INFORMATION:
NAME: Hanson, No. 5840568man D.
REGISTRATION NUMBER: 30,946
REFERENCE/DOCKET NUMBER: LUD 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    176 euArgAsnLysLeuLeuGluCysSerMetLysTyrAsnPheAspPheGlu 192
                                                                                                                                                                                                                                                                                                                                 TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM: MEDIUM TYPE: Diskett
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CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: Hodgkin's Di
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: Felfe & Lynch
STREET: 805 Third Avenue
CITY: New York City
                                                                                                                                                                              STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: 08/6 FILING DATE: 10-MAY-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OPERATING SYSTEM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ValGluAspValGluSerArgArgArgLeuArgLysSerLeuHisGluTh 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /cgn2_6/ptodata/2/ina/5B_COMB.seq:US-08-668-128B-7
                           Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New York
                                                                                                                                                                                                                                                                                        (212)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MALLOW, Michael Freundschuh, Michael Priceundschuh, Michael Propries And VENTION: Hodgkin's Disease Associated Molecules And
                                                                                                                                                     linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MBI
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                                                                                                                                                                                                                                                                                                            (212) 688-9200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Diskette, 3.5 inch, 360 kb storage
                                                                                                                                                                              single
  96.50
0.791
54.955
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               08/479,328
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Percent Identity: 20.270
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                                               Length:
                      Gaps:
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seq_documentation_block:
; Sequence 7, Application US/08905445
; Patent No. 5864015
                                                                                                                                                                                                                                                                                                                                seq_name: /cgn2_6/ptodata/2/ina/5B_COMB.seq:US-08-905-445-7
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US-09-574-735C-2 x US-08-668-128B-7
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                                                                                                                                                                                 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                            1807 GAGAGAAGAGCAGCTG 1822
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1757
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1193 CTGGAAGCCATCAGGTCGAAACTGGACAAAGCAGAAGACCAGCATCTCGT 1242
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                                                                                     APPLICANT: Pfreundschuh, Michael
TITLE OF INVENTION: Hodgkin's Disease Associated Molecules And
TITLE OF INVENTION: Uses Thereof
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            162 luAlaGluLeuGluAspPhePheGlnValAlaGluLysAsp..... 175
                         NUMBER OF SEQUENCES: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                80 CysGlnIleGluGluGluAspSerSerValSerCysCysSerThrSerG1 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        66 alIleValArgArgArgAspSerProProValGluGluGln...... 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  34 alGluSerArgIleIleLeuSerProCysValGlnAlaThr..... 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 MetAlaAlaValArgArgArgGluArgAspValValGluGluAsnGlyVa 17
   ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              uGluLysSerLysArgArgIleGluPheValAspLeuGluGluAsnAsnG 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CTGAGAGAAAACTTAGCAGATATGGAGGCAAAATTTAGAGAGAAAGATGA 1806
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              lGluSerArgArgArgLeuArgLysSerLeuHisGluThrVal...LysG 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TGATGCACTTCGGAAAGCCAGTTCCGAAGGTAAATCGGAAATGAAGAAAC 1442
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       lThrThrThrThrValLysArgArgLysMetGluGluValAspLeuV 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                     uLysAspGluProLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LeuArgAsnLysLeuLeuGluCysSerMetLysTyrAsnPheAspPheGl 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CTCT.....GTTCAGAGAAGTATGCAAGAAACTGTAAATAAGT 1706
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GAACTTCAGATTTTGAAAGAAAAGTTTGCTGAAGCTTCAGAGGAGGCAGT 1668
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SerGluGluSerMetAsnMetAspSerSerSerValAlaValGluAspVa 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     lyAspAspArgGluThrGluThrSerTrpIleTyrAspAspLeuAsnLys 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AGAGCTCCAGGGGAGAGAGCTAAAGCTTACTAACCTTCAGGAAAAT.... 1579
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TT....AGACAGCAGCTTGAGGCAGCTGAGAAACAGATTAAACAT 1483
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 gGlyGlyIleValAlaArgAsnSerAlaGlyAlaSerGluThrSerValV 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Felfe & Lynch
                                                                                                                                                                                                                                                                                                                                                                                                                                                        197
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TOPOLOGY: US-08-905-445-7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Align seg 1/1 to: US-08-905-445-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-574-735C-2 x US-08-905-445-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE: 10-MAY-1996
PRIOR APPLICATION NUMBER: 08/580,980
FILING DATE: 03-JANUARY-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/479,328
FILING DATE: 07-JUNE-1995
ATTORNEY/ACENT INFORMATION:
NAME: HANSON, NO. 5864015man D.
REGISTRATION NUMBER: 30,946
REGISTRATION NUMBER: 30,946
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: (212) 838-38 INFORMATION FOR SEQ ID NO:
1443 TT.....AGACAGCAGCTTGAGGCAGCTGAGAAACAGATTAAACAT 1483
                                                                                                                                                                                                                                                                                     1293 AGGAGCTAGAGGTACTGCAAGCCAAATGCAATGAACAAACCAAGGTTATT 1342
                                                                                                                                                                                                                                                                                                                                                                                 1243 AGAAATGGAAGACACGTTAAACAAATTACAGGAAGCTGAAATAAAGGTAA 1292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1193 CTGGAAGCCATCAGGTCGAAACTGGACAAAGCAGAAGACCAGCATCTCGT 1242
                                                                                                                                                                                         1343 GATAATTTTACATCACAGCTCAAGGCTACTGAAGAAAAGCTCTTGGATCT 1392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER: LUTELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OPERATING SYSTEM: PC-DOS SOFTWARE: Wordperfect CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CITY: New York City
STATE: New York
ZIP: 10022
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                               34 alGluSerArgIleIleLeuSerProCysValGlnAlaThr..... 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
                                            66 allleValArgArgArgAspSerProProValGluGluGln.....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 MetAlaAlaValArgArgArgGluArgAspValValGluGluAsnGlyVa 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: 08/668,128 FILING DATE: 21-JUNE-1996 APPLICATION NUMBER: 08/644,116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/08/905,445 FILING DATE: 04-AUG-1997 CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDIUM TYPE: Diskette, 3.5 inch, 360 kb storage
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                                                                                           TGATGCACTTCGGAAAGCCAGTTCCGAAGGTAAATCGGAAATGAAGAAAC
                                                                                                                                     gGlyGlyIleValAlaArgAsnSerAlaGlyAlaSerGluThrSerValV 66
                                                                                                                                                                                                                                                                                                                                                                                                                           lThrThrThrValLysArgArgLysMetGluGluValAspLeuV 34
                                                                                                                                                                                                                         ......AsnAr 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Quality:
Ratio:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (212) 688-9200
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0.791
54.955
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                                                                                           1442
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seq_documentation_block:
; Sequence 67, Applicati
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                                                                                                                                                                                                                                                                   COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, V6
CURRENT APPLICATION DATA:
APPLICATION UNMBER: US/08/235,836C
FILING DATE: 29-APR-1994
CLASSIFICATION: 435
                       TELEFAX: (516) 282-37 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           tent No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1534
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1484 TTAGAGATTGAAAAGAATGCTGAAAGTAGCAAGGCTAGTAGCATTACCAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       130
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      113 lyAspAspArgGluThrGluThrSerTrpIleTyrAspAspLeuAsnLys 129
                                                               TELEPHONE: (516) 282-7338
                                                                                                                                                                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/148,191
FILING DATE: 01-11-93
                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          176 LeuargasnLysLeuLeuGluCysSerMetLysTyrasnPheAspPheGl 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT:
                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: No. 6248562el Chimeric Proteins Comprising
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES:
                                                                                                                NAME: Bogosian, Margaret C. REGISTRATION NUMBER: 25,324 REFERENCE/DOCKET NUMBER: BN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CITY: Upton
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: Brookhaven National Laboratory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              luAlaGluLeuGluAspPhePheGlnValAlaGluLysAsp...... 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AGAGCTCCAGGGGAGAGACCTAAAGCTTACTAACCTTCAGGAAAAT.... 1579
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   uLysAspGluProLeu 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CTGAGAGAAAACTTAGCAGATATGGAGGCAAAATTTAGAGAGAAAAGATGA 1806
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CTCT.....GTTCAGAGAAGTATGCAAGAAACTGTAAATAAGT 1706
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SerGluGluSerMetAsnMetAspSerSerSerValAlaValGluAspVa 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CysGlnIleGluGluAspSerSerValSerCysCysSerThrSerGl
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      USA
                                          (516)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Dunn, John J.
Luft, Benjamin J.
                                          282-3729
                                                                                                                                                                                                                                                                                                                    US/08/235,836C
                         67:
                                                                                                                BNL93-28A
                                                                                                                                                                                                                                                                                                                                                                Version
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alignment_block:
US-09-574-735C-2 x US-08-235-836C-67
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Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-08-235-836C-67
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                                          1408
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             120 rSerTrpIleTyrAspAspLeuAsnLysSerGluGluSerMetAsnMetA 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             104 GluPheValAspLeuGluGluAsnAsnGlyAspAspArgGluThrGluTh 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           916 CAACAAAATTAGATTCTTCTGAAGATAATTTAGATATTCAAAGGGATAC
194 pGluProLeu 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     966 TGTTAGAGAGAAGATTCAAGAGGATATTGACGAGATTAATAAAGAA.... 1011
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          56 AsnSerAlaGlyAlaSerGluThrSerValValIleValArgArgArgAs 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             39 leLeuSerProCysValGlnAlaThrAsnArgGlyGlyIleValAlaArg 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                22 lLysArgArgLysMetGluGluGluValAspLeuValGluSerArgIleI 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY:
LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6 ArgArgGluArgAspValValGluGluAsnGlyValThrThrThrThrVa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY:
                                          GAGAGAGTAAATGAAATTTCGAAGTCTAACAACAATGAGATTAGTGAATC 1457
                                                                                                                                                                                                                                                                                                                                           LysSerLeuHisGluThrValLysGlu......AlaGl 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      erSerValSerCysCysSerThrSerGluGluLysSerLysArgArgIle 103
                                                                                 AsnLysLeuLeuGluCysSerMetLysTyrAsnPheAspPheGluLysAs
                                                                                                                                AGGATAAAAATTAGATAGTAAAAAAAATTTAAAACCTGTTTCTGAGATT 1407
                                                                                                                                                                    luAspPhePheGlnValAlaGluLysAspLeuArg......
                                                                                                                                                                                                                     TTTGAATAATGACGAAAATCTTATGAGGCCGGAAGATCAAAAATTATCTG 1357
                                                                                                                                                                                                                                                                                                         GGCAAAGAAGGAGAAATAGTCAAAGAGGAATCAAAGGCAAGTTTAGCTGA 1307
                                                                                                                                                                                                                                                                                                                                                                                                                       spSerSerSerValAlaValGluAspValGluSerArgArgArgLeuArg 153
|| ::::::
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CAAAAAAAGTGATGAAGAACTTTTAAAAAGTAAAGATCCTAAAGCATTAG 1207
                                                                                                                                                                                                                                                                                                                                                                                              ATCTTAATGGAGATTTAAATTCTAAAGTTTCTAGTAAAGAAAAAATTAAA 1257
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0.889
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   from: 1
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alignment_block:
US-09-574-735C-2 x US-08-836-567-11
                                                                                                                                             alignment_scores:
                                                                                                                                                                                                   ; NAME/KEY:
; LOCATION:
US-08-836-567-11
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                                                                                          Ratio:
Percent Similarity:
Align seg 1/1 to: US-08-836-567-11 from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: KOSSMANN, Jens
APPLICANT: Springer, Franziska
APPLICANT: Abel, Gernot
TITLE OF INVENTION: DNA MOLECULE
TITLE OF INVENTION: INVOLVED IN
TITLE OF INVENTION: PLANT CELLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ::::||||||
1458 ATCACCATTA 1467
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            tent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOETWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/I
FILING DATE: 09-NOV-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                            FEATURE:
                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE:
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELECOMMUNICATION INFORMATION: TELEPHONE: 212-596-9000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE P 44 41 408.0
FILING DATE: 10-NOV-1994
                                                                                                                                                                                                                                                                                           IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                               ORGANISM:
STRAIN: 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STREET: 1251 Avenue of the Americas CITY: New York
STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/08/836,567 FILING DATE: 24-JUL-1997
                                                                                                                                                                                                                                                                                                              STRAIN: cv. Dsire
TISSUE TYPE: leaf
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: Agrevo-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Haley Jr., James F. REGISTRATION NUMBER: 27,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY: UZIP: 10020
                                                                                                                                                                                                                                                                          LIBRARY: cDNA-library in Lambda ZAPII
                                                                                                                                                                                                                                                                                                                                                                                                                      STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                            ENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /cgn2_6/ptodata/2/ina/6A_COMB.seq:US-08-836-567-11
                                                                                                                              Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                         nucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Application US/08836567
                                                                                                                                                                                                                                                                                                                                                                                                                                                    4168 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   212-596-9090
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                                                                                                                                                                                                                                                                                                                                                 Solanum tuberosum
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307..3897
                                                                                                                                                                                                                                                                                                                                                                                                  linear
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                                                                                                                                                                                                                                                                                                                                                                                   cDNA to RNA
                                                                                                                                                                                                                                                                                                              leaf tissue
                                                                                                                                                                                                                                                                                                                                                                                                                    single
                                                                                        96.00
0.800
48.780
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DNA MOLECULES THAT CODE FOR ENZYMES INVOLVED IN STARCH SYNTHESIS VECTORS BACTERIA TRANSGENIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PCT/EP95/04415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                11:
                                                                                          Percent
                                                                                          Identity:
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Gaps:
to: 4168
                                                                                        246
12
23.171
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seq_documentation_block:
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                                                                                    GENERAL INFORMATION:
                                                                                                               Patent No.
                                                                                                               Sequence 8, Application US/09153804 Patent No. 6207380
                        APPLICANT: Patricia Billing-Medel APPLICANT: Maurice Cohen
                                                                                                                                                                                                                                                                                     1070 TTGAAGAGGATGAGCCATTAGCTGCAGGAACAGTGGAG 1107
                                                                                                                                                                                                                                                                                                                                                                                                        1020 CAATGAGATTGATGACTTAGACACTAATAGTTTCTTTAAATCAGATTTAA 1069
                                                                                                                                                                                                                                                                                                                      970
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        776 GATCGGAAGAGAGTGATTTCTAATTGATTCTGTAATAAGAGAACAAAGT 825
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         132 luSerMetAsnMetAsp.....SerSerSerValAlaValGluAspVal 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        694 GTTCGTGTATCATCTCAATTTGTTGAAAGTGAAGAAACTGGTGGTGATGA 743
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       665 GTTCTACTAAATCAATAAGT........ATGTCACCT 693
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          624 G.....AGGGACCACAAGTTTCTGGAGGATGAAGGATGAAATCAATG 664
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          574 ACGGTTGAAGCAAGAGTTGAAACTAGTGACGATGACACTAAAGTAGTGGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   67
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Maurice Cohen
Paula N. Friedman
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V

APPLICANT:

APPLICANT:

Julian Gordon Steven C. Hodges Michael R. Klass

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FILE REFERENCE: 6180.US.01
CURRENT APPLICATION NUMBER: US/09/153,804
CURRENT FILING DATE: 1998-09-15
NUMBER OF SEQ ID NOS: 17
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 8
LENGTH: 1724
TYPE: DNA
ORGANISM: Homo Sapiens
US-09-153-804-8
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us-09-574-735C-2 x us-09-153-804-8
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Quality:
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APPLICANT: Eric Russell
APPLICANT: Stephen D. Stroupe
TITLE OF INVENTION: Reagents and Methods Useful for Detecting Diseases of the Urinary
TITLE OF INVENTION: Tract
                                                                                                                                                    1067
                                                                                                                                                                                               157
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                                                                                                                                                                                                                                                                                                                                                                    132 uSerMetAsnMetAsp.....SerSerS
103 leGluPheValAspLeuGluGlu......AsnAsnGlyAspAsp... 115
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               57 erAlaGlyAlaSerGluThrSerValValIle......ValArg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  40 uSerProCysValGlnAlaThrAsnArgGlyGlyIleValAlaArgAsnS
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                                                                                                                                                                                                                                                                          erValAlaValGluAspValGluSerArgArgArgLeuArgLysSerLeu 156
                                                                                                                                                                                                                                                                                                                                                                                                                                        ArgGluThrGluThrSerTrpIleTyrAspAspLeuAsnLysSerGluGl 132
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                                                                 CCTGCAGCGGGCCAAGCAGGACATGGCCCGGCAGCTGCGTGAGTACCAGG 1160
                                                                                                          ePheGlnValAlaGluLysAspLeuArgAsnLysLeuLeuGlu.....
                                                                                                                                                  .....GCCATTAAGGATGCCAACGCCAAGTTGTCCGAGCTGGAGGCCGC 1110
                                                                                                                                                                                             CCGGCTCCAGGCTGAGATTGAGGGCCTCAAAGGCCCAGAGGGCTTCCCTGG
                                                                                                                                                                                                                                                                                                                                                                                                               CGGCGCACAAAGACTGAG.....ATCTCAGAGATGAACCGGAACATCAG 978
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50.235
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Gaps: 11
Percent Identity: 22.535
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; NAME/KEY: CDS
; LOCATION: (1)..(5361)
US-08-973-462-2
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Patent No. 6191270
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APPLICANT: DAUBERSIES, PIERRE
APPLICANT: DAUBERSIES, PIERRE
APPLICANT: DAUBERSIES, PIERRE
ITILE OF INVENTION: MALAFIER PRE-ERYTHROCYTIC STAGE POLYPEPTIDE MOLECULES
FILE REFERENCE: 0660-0125-0 PCT
CURRENT FILING DATE: 1998-02-06
EARLIER APPLICATION NUMBER: PCT/FR96/00894
EARLIER APPLICATION NUMBER: PCT/FR96/00894
EARLIER APPLICATION NUMBER: PCT/FR96/007
EARLIER FILING DATE: 1996-06-13
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                                                                                                GluGlnCysGlnIleGluGluGlu...AspSerSerValSerCysCysSe 93
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3924	3924 TGTCGAAGAAGACAAGATCGAAAAAGTATCTGATTTAAAAGATCTTGAAG 3973	3973
110	110 luAsnAsnGlyAspAspArgGluThrGluThrSerTrpIleTyrAspAsp 126	126
3974	3974 AA	3981
127		143
3982	3982 TTAAAAGAAGTAAAAGAAATCAAAGAACTTGAAAGTGAAATTTT 4025	4025
143	143 lGluAspValGluSerArgArgArgLeuArgLysSerLeuHisGluThrV 160	160
4026	4026 AGAAGATTATAAAGAATTAAAAACTATTGAAACAGATATTTTAGAAGAGA 4075	4075
160	160 altysGluAlaGluLeuGluAspPhePheGlnValAlaGlu	173
4076	VAAGATCAT	4125
174	174LysAspLeuArgAsnLysLeuLeuGlu 182	
4126	4126 GAAATAAAAGATCTTGAAGCAGATATATTAAAA 4158	

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GGCAAATCATGAGTGTTTGGCTTCCTTGTTTGACAATGAAAGACAACATTTTCTGGGTCT 662
                                                                    GGAGAGTGAGGAGATTATCATGGAGATGGTGGAGAAGGAGGAGCAGCATTTGCCAAGTGA 182
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Pflanzenphysiologie, Universitaet Bayreuth, Universitaetsstr.
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1 (bases 1 to 1699)
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Nucleotide sequence of a cDNA encoding a D-type cyclin from a photoautotrophic cell suspension culture of Chenopodium rubium Plant Physiol. In press
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/product="cyclin-D like protein"
/protein_id="ChA71244 l"
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FLYKLSGDKMPSKSLIFQAIQLILSTIKGIDLMEFRPSEIAAAVALSVTQOTQIVEFT
DKAFSEITDHVEKERLMKCVEIMHDLRMSSRSNGALASTSVPQSPIGVLDASACLSYK
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/dev_stage="7 day old culture"
/clone_lib="lambda uniZAP-XR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                          /gene="cycD1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ACCATTTTCTTTCATAGACTATTTCCTTTATAAACTGAGT----GGAGATAAAATGCCATC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AATCCAAAGAATGGAACTTTTAGTGTTGAGCACTTTGAAGTGGAGAATGCAATCAGTGAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GATGATGCAATTGCTTGGGGTTGCTTGTTTATCTCTAGCTGCCAAGGTGGATGAAACTGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATCTGTAAACTACTTGGATCGCTTCCTTTCGGCTTATGAATTACC---TGGCAAAGCTTG
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Sequence 2
A85077
A85077.1
                                                                                                                                               MUTTAY, J.A.
PLANTS WITH MODIFIED GROWTH
PATENT: WO 9842851-A 21 01-OCT-1998;
MURRAY JAMES AUGUSTUS HENRY (GB); UN
                                                                                                                                                                                                                        Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC
clade; Panicoideae; Andropogoneae; Zea.
                                                                                                                                                                                                                                                                                     2ea mays
                                                                                                                                                                                                             (bases 1 to 1846)
                                                                           448
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                                                                       /organism="Zea mays"
/db_xref="taxon:4577"
425 c 514 g
                                                                                                                                    Location/Qualifiers
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20.9%;
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Score 193.4; DB 6;
Pred. No. 4.4e-38;
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            Length 1846;
                                                                           others
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Query Match
Best Local Similarity
Matches 364; Conserv

Conservative

0

Mismatches 236;

Indels

9

Gaps

THE HAKE BLANK (USPID)